

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Lal, Preeti
Hillman, Jennifer L.
Corley, Neil C.
Guegler, Karl J.
Baugh, Mariah
Sather, Susan
Shah, Purvi

(ii) TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS

(iii) NUMBER OF SEQUENCES:154

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
(B) STREET: 3174 PORTER DRIVE
(C) CITY: PALO ALTO
(D) STATE: CALIFORNIA
(E) COUNTRY: USA
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: TO BE ASSIGNED
(B) FILING DATE: HERewith
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: BILLINGS, LUCY J.
(B) REGISTRATION NUMBER: 36,749
(C) REFERENCE/DOCKET NUMBER:PF-0459 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (650) 855-0555
(B) TELEFAX: (650) 845-4166

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 348 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

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(A) LIBRARY: HEARNOT01

(B) CLONE: 305841

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1 :

Met	Ala	Ala	Thr	Leu	Gly	Pro	Leu	Gly	Ser	Trp	Gln	Gln	Trp	Arg	
				5					10					15	
Arg	Cys	Leu	Ser	Ala	Arg	Asp	Gly	Ser	Arg	Met	Leu	Leu	Leu	Leu	
				20					25					30	
Leu	Leu	Leu	Gly	Ser	Gly	Gln	Gly	Pro	Gln	Gln	Val	Gly	Ala	Gly	
				35					40					45	
Gln	Thr	Phe	Glu	Tyr	Leu	Lys	Arg	Glu	His	Ser	Leu	Ser	Lys	Pro	
				50					55					60	
Tyr	Gln	Gly	Val	Gly	Thr	Gly	Ser	Ser	Ser	Leu	Trp	Asn	Leu	Met	
				65					70					75	
Gly	Asn	Ala	Met	Val	Met	Thr	Gln	Tyr	Ile	Arg	Leu	Thr	Pro	Asp	
				80					85					90	
Met	Gln	Ser	Lys	Gln	Gly	Ala	Leu	Trp	Asn	Arg	Val	Pro	Cys	Phe	
				95					100					105	
Leu	Arg	Asp	Trp	Glu	Leu	Gln	Val	His	Phe	Lys	Ile	His	Gly	Gln	
				110					115					120	
Gly	Lys	Lys	Asn	Leu	His	Gly	Asp	Gly	Leu	Ala	Ile	Trp	Tyr	Thr	
				125					130					135	
Lys	Asp	Arg	Met	Gln	Pro	Gly	Pro	Val	Phe	Gly	Asn	Met	Asp	Lys	
				140					145					150	
Phe	Val	Gly	Leu	Gly	Val	Phe	Val	Asp	Thr	Tyr	Pro	Asn	Glu	Glu	
				155					160					165	
Lys	Gln	Gln	Glu	Arg	Val	Phe	Pro	Tyr	Ile	Ser	Ala	Met	Val	Asn	
				170					175					180	
Asn	Gly	Ser	Leu	Ser	Tyr	Asp	His	Glu	Arg	Asp	Gly	Arg	Pro	Thr	
				185					190					195	
Glu	Leu	Gly	Gly	Cys	Thr	Ala	Ile	Val	Arg	Asn	Leu	His	Tyr	Asp	
				200					205					210	
Thr	Phe	Leu	Val	Ile	Arg	Tyr	Val	Lys	Arg	His	Leu	Thr	Ile	Met	
				215					220					225	
Met	Asp	Ile	Asp	Gly	Lys	His	Glu	Trp	Arg	Asp	Cys	Ile	Glu	Val	
				230					235					240	
Pro	Gly	Val	Arg	Leu	Pro	Arg	Gly	Tyr	Tyr	Phe	Gly	Thr	Ser	Ser	
				245					250					255	
Ile	Thr	Gly	Asp	Leu	Ser	Asp	Asn	His	Asp	Val	Ile	Ser	Leu	Lys	
				260					265					270	
Leu	Phe	Glu	Leu	Thr	Val	Glu	Arg	Thr	Pro	Glu	Glu	Glu	Lys	Leu	
				275					280					285	
His	Arg	Asp	Val	Phe	Leu	Pro	Ser	Val	Asp	Asn	Met	Lys	Leu	Pro	
				290					295					300	
Glu	Met	Thr	Ala	Pro	Leu	Pro	Pro	Leu	Ser	Gly	Leu	Ala	Leu	Phe	
				305					310					315	
Leu	Ile	Val	Phe	Phe	Ser	Leu	Val	Phe	Ser	Val	Phe	Ala	Ile	Val	
				320					325					330	
Ile	Gly	Ile	Ile	Leu	Tyr	Asn	Lys	Trp	Gln	Glu	Gln	Ser	Arg	Lys	
				335					340					345	
Arg	Phe	Tyr													

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 194 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: EOSIHET02
(B) CLONE: 322866

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2 :

Met	Gly	Met	Ser	Ser	Leu	Lys	Leu	Leu	Lys	Tyr	Val	Leu	Phe	Phe	5	10	15
Phe	Asn	Leu	Leu	Phe	Trp	Ile	Cys	Gly	Cys	Cys	Ile	Leu	Gly	Phe	20	25	30
Gly	Ile	Tyr	Leu	Leu	Ile	His	Asn	Asn	Phe	Gly	Val	Leu	Phe	His	35	40	45
Asn	Leu	Pro	Ser	Leu	Thr	Leu	Gly	Asn	Val	Phe	Val	Ile	Val	Gly	50	55	60
Ser	Ile	Ile	Met	Val	Val	Ala	Phe	Leu	Gly	Cys	Met	Gly	Ser	Ile	65	70	75
Lys	Glu	Asn	Lys	Cys	Leu	Leu	Met	Ser	Phe	Phe	Ile	Leu	Leu	Leu	80	85	90
Ile	Ile	Leu	Leu	Ala	Glu	Val	Thr	Leu	Ala	Ile	Leu	Leu	Phe	Val	95	100	105
Tyr	Glu	Gln	Lys	Leu	Asn	Glu	Tyr	Val	Ala	Lys	Gly	Leu	Thr	Asp	110	115	120
Ser	Ile	His	Arg	Tyr	His	Ser	Asp	Asn	Ser	Thr	Lys	Ala	Ala	Trp	125	130	135
Asp	Ser	Ile	Gln	Ser	Phe	Leu	Gln	Cys	Cys	Gly	Ile	Asn	Gly	Thr	140	145	150
Ser	Asp	Leu	Asp	Ser	Gly	Ser	Pro	Ala	Ser	Cys	Pro	Ser	Asp	Arg	155	160	165
Lys	Val	Glu	Gly	Cys	Tyr	Ala	Lys	Glu	Asp	Phe	Gly	Phe	Ile	Gln	170	175	180
Phe	Pro	Val	Tyr	Arg	Asn	His	His	His	Leu	Cys	Met	Cys	Asp		185	190	

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 342 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: BEPINOT01
(B) CLONE: 546656

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3 :

Met	Ser	Leu	His	Gly	Lys	Arg	Lys	Glu	Ile	Tyr	Lys	Tyr	Glu	Ala	5	10	15
Pro	Trp	Thr	Val	Tyr	Ala	Met	Asn	Trp	Ser	Val	Arg	Pro	Asp	Lys	20	25	30
Arg	Phe	Arg	Leu	Ala	Leu	Gly	Ser	Phe	Val	Glu	Glu	Tyr	Asn	Asn	35	40	45
Lys	Val	Gln	Leu	Val	Gly	Leu	Asp	Glu	Glu	Ser	Ser	Glu	Phe	Ile	50	55	60

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Cys	Arg	Asn	Thr	Phe	Asp	His	Pro	Tyr	Pro	Thr	Thr	Lys	Leu	Met
				65					70					75
Trp	Ile	Pro	Asp	Thr	Lys	Gly	Val	Tyr	Pro	Asp	Leu	Leu	Ala	Thr
				80					85					90
Ser	Gly	Asp	Tyr	Leu	Arg	Val	Trp	Arg	Val	Gly	Glu	Thr	Glu	Thr
				95					100					105
Arg	Leu	Glu	Cys	Leu	Leu	Asn	Asn	Asn	Lys	Asn	Ser	Asp	Phe	Cys
				110					115					120
Ala	Pro	Leu	Thr	Ser	Phe	Asp	Trp	Asn	Glu	Val	Asp	Pro	Tyr	Leu
				125					130					135
Leu	Gly	Thr	Ser	Ser	Ile	Asp	Thr	Thr	Cys	Thr	Ile	Trp	Gly	Leu
				140					145					150
Glu	Thr	Gly	Gln	Val	Leu	Gly	Arg	Val	Asn	Leu	Val	Ser	Gly	His
				155					160					165
Val	Lys	Thr	Gln	Leu	Ile	Ala	His	Asp	Lys	Glu	Val	Tyr	Asp	Ile
				170					175					180
Ala	Phe	Ser	Arg	Ala	Gly	Gly	Gly	Arg	Asp	Met	Phe	Ala	Ser	Val
				185					190					195
Gly	Ala	Asp	Gly	Ser	Val	Arg	Met	Phe	Asp	Leu	Arg	His	Leu	Glu
				200					205					210
His	Ser	Thr	Ile	Ile	Tyr	Glu	Asp	Pro	Gln	His	His	Pro	Leu	Leu
				215					220					225
Arg	Leu	Cys	Trp	Asn	Lys	Gln	Asp	Pro	Asn	Tyr	Leu	Ala	Thr	Met
				230					235					240
Ala	Met	Asp	Gly	Met	Glu	Val	Val	Ile	Leu	Asp	Val	Arg	Val	Pro
				245					250					255
Cys	Thr	Pro	Val	Ala	Arg	Leu	Asn	Asn	His	Arg	Ala	Cys	Val	Asn
				260					265					270
Gly	Ile	Ala	Trp	Ala	Pro	His	Ser	Ser	Cys	His	Ile	Cys	Thr	Ala
				275					280					285
Ala	Asp	Asp	His	Gln	Ala	Leu	Ile	Trp	Asp	Ile	Gln	Gln	Met	Pro
				290					295					300
Arg	Ala	Ile	Glu	Asp	Pro	Ile	Leu	Ala	Tyr	Thr	Ala	Glu	Gly	Glu
				305					310					315
Ile	Asn	Asn	Val	Gln	Trp	Ala	Ser	Thr	Gln	Pro	Asp	Trp	Ile	Ala
				320					325					330
Ile	Cys	Tyr	Asn	Asn	Cys	Leu	Glu	Ile	Leu	Arg	Val			
				335					340					

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 656 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SYNORAT03
- (B) CLONE: 693453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4 :

Met	Glu	Glu	Leu	Asp	Gly	Glu	Pro	Thr	Val	Thr	Leu	Ile	Pro	Gly
				5					10					15
Val	Asn	Ser	Lys	Lys	Asn	Gln	Met	Tyr	Phe	Asp	Trp	Gly	Pro	Gly
				20					25					30
Glu	Met	Leu	Val	Cys	Glu	Thr	Ser	Phe	Asn	Lys	Lys	Glu	Lys	Ser

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				35					40					45
Glu	Met	Val	Pro	Ser	Cys	Pro	Phe	Ile	Tyr	Ile	Ile	Arg	Lys	Asp
				50					55					60
Val	Asp	Val	Tyr	Ser	Gln	Ile	Leu	Arg	Lys	Leu	Phe	Asn	Glu	Ser
				65					70					75
His	Gly	Ile	Phe	Leu	Gly	Leu	Gln	Arg	Ile	Asp	Glu	Glu	Leu	Thr
				80					85					90
Gly	Lys	Ser	Arg	Lys	Ser	Gln	Leu	Val	Arg	Val	Ser	Lys	Asn	Tyr
				95					100					105
Arg	Ser	Val	Ile	Arg	Ala	Cys	Met	Glu	Glu	Met	His	Gln	Val	Ala
				110					115					120
Ile	Ala	Ala	Lys	Asp	Pro	Ala	Asn	Gly	Arg	Gln	Phe	Ser	Ser	Gln
				125					130					135
Val	Ser	Ile	Leu	Ser	Ala	Met	Glu	Leu	Ile	Trp	Asn	Leu	Cys	Glu
				140					145					150
Ile	Leu	Phe	Ile	Glu	Val	Ala	Pro	Ala	Gly	Pro	Leu	Leu	Leu	His
				155					160					165
Leu	Leu	Asp	Trp	Val	Arg	Leu	His	Val	Cys	Glu	Val	Asp	Ser	Leu
				170					175					180
Ser	Ala	Asp	Val	Leu	Gly	Ser	Glu	Asn	Pro	Ser	Lys	His	Asp	Ser
				185					190					195
Phe	Trp	Asn	Leu	Val	Thr	Ile	Leu	Val	Leu	Gln	Gly	Arg	Leu	Asp
				200					205					210
Glu	Ala	Arg	Gln	Met	Leu	Ser	Lys	Glu	Ala	Asp	Ala	Ser	Pro	Ala
				215					220					225
Ser	Ala	Gly	Ile	Cys	Arg	Ile	Met	Gly	Asp	Leu	Met	Arg	Thr	Met
				230					235					240
Pro	Ile	Leu	Ser	Pro	Gly	Asn	Thr	Gln	Thr	Leu	Thr	Glu	Leu	Glu
				245					250					255
Leu	Lys	Trp	Gln	His	Trp	His	Glu	Glu	Cys	Glu	Arg	Tyr	Leu	Gln
				260					265					270
Asp	Ser	Thr	Phe	Ala	Thr	Ser	Pro	His	Leu	Glu	Ser	Leu	Leu	Lys
				275					280					285
Ile	Met	Leu	Gly	Asp	Glu	Ala	Ala	Leu	Leu	Glu	Gln	Lys	Glu	Leu
				290					295					300
Leu	Ser	Asn	Trp	Tyr	His	Phe	Leu	Val	Thr	Arg	Leu	Leu	Tyr	Ser
				305					310					315
Asn	Pro	Thr	Val	Lys	Pro	Ile	Asp	Leu	His	Tyr	Tyr	Ala	Gln	Ser
				320					325					330
Ser	Leu	Asp	Leu	Phe	Leu	Gly	Gly	Glu	Ser	Ser	Pro	Glu	Pro	Leu
				335					340					345
Asp	Asn	Ile	Leu	Leu	Ala	Ala	Phe	Glu	Phe	Asp	Ile	His	Gln	Val
				350					355					360
Ile	Lys	Glu	Cys	Ser	Ile	Ala	Leu	Ser	Asn	Trp	Trp	Phe	Val	Ala
				365					370					375
His	Leu	Thr	Asp	Leu	Leu	Asp	His	Cys	Lys	Leu	Leu	Gln	Ser	His
				380					385					390
Asn	Leu	Tyr	Phe	Gly	Ser	Asn	Met	Arg	Glu	Phe	Leu	Leu	Leu	Glu
				395					400					405
Tyr	Ala	Ser	Gly	Leu	Phe	Ala	His	Pro	Ser	Leu	Trp	Gln	Leu	Gly
				410					415					420
Val	Asp	Tyr	Phe	Asp	Tyr	Cys	Pro	Glu	Leu	Gly	Arg	Val	Ser	Leu
				425					430					435
Glu	Leu	His	Ile	Glu	Arg	Ile	Pro	Leu	Asn	Thr	Glu	Gln	Lys	Ala
				440					445					450
Leu	Lys	Val	Leu	Arg	Ile	Cys	Glu	Gln	Arg	Gln	Met	Thr	Glu	Gln
				455					460					465
Val	Arg	Ser	Ile	Cys	Lys	Ile	Leu	Ala	Met	Lys	Ala	Val	Arg	Asn
				470					475					480
Asn	Arg	Leu	Gly	Ser	Ala	Leu	Ser	Trp	Ser	Ile	Arg	Ala	Lys	Asp
				485					490					495

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Ala	Ala	Phe	Ala	Thr	Leu	Val	Ser	Asp	Arg	Phe	Leu	Arg	Asp	Tyr
				500					505					510
Cys	Glu	Arg	Gly	Cys	Phe	Ser	Asp	Leu	Asp	Leu	Ile	Asp	Asn	Leu
				515					520					525
Gly	Pro	Ala	Met	Met	Leu	Ser	Asp	Arg	Leu	Thr	Phe	Leu	Gly	Lys
				530					535					540
Tyr	Arg	Glu	Phe	His	Arg	Met	Tyr	Gly	Glu	Lys	Arg	Phe	Ala	Asp
				545					550					555
Ala	Ala	Ser	Leu	Leu	Leu	Ser	Leu	Met	Thr	Ser	Arg	Ile	Ala	Pro
				560					565					570
Arg	Ser	Phe	Trp	Met	Thr	Leu	Leu	Thr	Asp	Ala	Leu	Pro	Leu	Leu
				575					580					585
Glu	Gln	Lys	Gln	Val	Ile	Phe	Ser	Ala	Glu	Gln	Thr	Tyr	Glu	Leu
				590					595					600
Met	Arg	Cys	Leu	Glu	Asp	Leu	Thr	Ser	Arg	Arg	Pro	Val	His	Gly
				605					610					615
Glu	Ser	Asp	Thr	Glu	Gln	Leu	Gln	Asp	Asp	Asp	Ile	Glu	Thr	Thr
				620					625					630
Lys	Val	Glu	Met	Leu	Arg	Leu	Ser	Leu	Ala	Arg	Asn	Leu	Ala	Arg
				635					640					645
Ala	Ile	Ile	Arg	Glu	Gly	Ser	Leu	Glu	Gly	Ser				
				650					655					

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAITUT03
- (B) CLONE: 866885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5 :

Met	Ala	Pro	Asp	Pro	Trp	Phe	Ser	Thr	Tyr	Asp	Ser	Thr	Cys	Gln
				5					10					15
Ile	Ala	Gln	Glu	Ile	Ala	Glu	Lys	Ile	Gln	Gln	Arg	Asn	Gln	Tyr
				20					25					30
Glu	Arg	Lys	Gly	Glu	Lys	Ala	Pro	Lys	Leu	Thr	Val	Thr	Ile	Arg
				35					40					45
Ala	Leu	Leu	Gln	Asn	Leu	Lys	Glu	Lys	Ile	Ala	Leu	Leu	Lys	Asp
				50					55					60
Leu	Leu	Leu	Arg	Ala	Val	Ser	Thr	His	Gln	Ile	Thr	Gln	Leu	Glu
				65					70					75
Gly	Asp	Arg	Arg	Gln	Asn	Leu	Leu	Asp	Asp	Leu	Val	Thr	Arg	Glu
				80					85					90
Arg	Leu	Leu	Leu	Ala	Ser	Phe	Lys	Asn	Glu	Gly	Ala	Glu	Pro	Asp
				95					100					105
Leu	Ile	Arg	Ser	Ser	Leu	Met	Ser	Glu	Glu	Ala	Lys	Arg	Gly	Ala
				110					115					120
Pro	Asn	Pro	Trp	Leu	Phe	Glu	Glu	Pro	Glu	Glu	Thr	Arg	Gly	Leu
				125					130					135
Gly	Phe	Asp	Glu	Ile	Arg	Gln	Gln	Gln	Gln	Lys	Ile	Ile	Gln	Glu
				140					145					150
Gln	Asp	Ala	Gly	Leu	Asp	Ala	Leu	Ser	Ser	Ile	Ile	Ser	Arg	Gln

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Lys	Gln	Met	Gly	155	Gln	Glu	Ile	Gly	Asn	160	Glu	Leu	Asp	Glu	Gln	Asn	165
				170						175							180
Glu	Ile	Ile	Asp	185	Asp	Leu	Ala	Asn	Leu	190	Val	Glu	Asn	Thr	Asp	Glu	195
Lys	Leu	Arg	Asn	200	Glu	Thr	Arg	Arg	Val	205	Asn	Met	Val	Asp	Arg	Lys	210
Ser	Ala	Ser	Cys	215	Gly	Met	Ile	Met	Val	220	Ile	Leu	Leu	Leu	Leu	Val	225
Ala	Ile	Val	Val	230	Val	Ala	Val	Trp	Pro	235	Thr	Asn					

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: LUNGNOT03

(B) CLONE: 1242271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6 :

Met	Leu	Leu	Asp	Thr	Val	Gln	Lys	Val	Phe	Gln	Lys	Met	Leu	Glu			
				5					10					15			
Cys	Ile	Ala	Arg	Ser	Phe	Arg	Lys	Gln	Pro	Glu	Glu	Gly	Leu	Arg			
				20					25					30			
Leu	Leu	Tyr	Ser	Val	Gln	Arg	Pro	Leu	His	Glu	Phe	Ile	Thr	Ala			
				35					40					45			
Val	Gln	Ser	Arg	His	Thr	Asp	Thr	Pro	Val	His	Arg	Gly	Val	Leu			
				50					55					60			
Ser	Thr	Leu	Ile	Ala	Gly	Pro	Val	Val	Glu	Ile	Ser	His	Gln	Leu			
				65					70					75			
Arg	Lys	Val	Ser	Asp	Val	Glu	Glu	Leu	Thr	Pro	Pro	Glu	His	Leu			
				80					85					90			
Ser	Asp	Leu	Pro	Pro	Phe	Ser	Arg	Cys	Leu	Ile	Gly	Ile	Ile	Ile			
				95					100					105			
Lys	Ser	Ser	Asn	Val	Val	Arg	Ser	Phe	Leu	Asp	Glu	Leu	Lys	Ala			
				110					115					120			
Cys	Val	Ala	Ser	Asn	Asp	Ile	Glu	Gly	Ile	Val	Cys	Leu	Thr	Ala			
				125					130					135			
Ala	Val	His	Ile	Ile	Leu	Val	Ile	Asn	Ala	Gly	Lys	His	Lys	Ser			
				140					145					150			
Ser	Lys	Val	Arg	Glu	Val	Ala	Ala	Thr	Val	His	Arg	Lys	Leu	Lys			
				155					160					165			
Thr	Phe	Met	Glu	Ile	Thr	Leu	Glu	Glu	Asp	Ser	Ile	Glu	Arg	Phe			
				170					175					180			
Leu	Tyr	Glu	Ser	Ser	Ser	Arg	Thr	Leu	Gly	Glu	Leu	Leu	Asn	Ser			
				185					190					195			

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGFET03
- (B) CLONE: 1255027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7 :

Met	Thr	Lys	Thr	Asp	Glu	Thr	Thr	Leu	Val	Ala	Ser	Trp	Glu	Thr	5	10	15
Arg	Glu	Lys	Thr	Ala	Lys	Thr	Thr	Leu	Phe	Leu	Pro	Leu	Glu	Phe	20	25	30
Trp	Ser	Tyr	Lys	Ala	Glu	Val	Pro	His	Leu	Pro	Glu	Leu	Ala	Tyr	35	40	45
Ser	Ala	Arg	Ser	Lys	Met	Ala	Glu	Leu	Asn	Thr	His	Val	Asn	Val	50	55	60
Lys	Glu	Lys	Ile	Tyr	Ala	Val	Arg	Ser	Val	Val	Pro	Asn	Lys	Ser	65	70	75
Asn	Asn	Glu	Ile	Val	Leu	Val	Leu	Gln	Gln	Phe	Asp	Phe	Asn	Val	80	85	90
Asp	Lys	Ala	Val	Gln	Ala	Phe	Val	Asp	Gly	Ser	Ala	Ile	Gln	Val	95	100	105
Leu	Lys	Glu	Trp	Asn	Met	Thr	Gly	Lys	Lys	Lys	Asn	Asn	Lys	Arg	110	115	120
Lys	Arg	Ser	Lys	Ser	Lys	Gln	His	Gln	Gly	Asn	Lys	Asp	Ala	Lys	125	130	135
Asp	Lys	Val	Glu	Arg	Pro	Glu	Ala	Gly	Pro	Leu	Gln	Pro	Gln	Pro	140	145	150
Pro	Gln	Ile	Gln	Asn	Gly	Pro	Met	Asn	Gly	Cys	Glu	Lys	Asp	Ser	155	160	165
Ser	Ser	Thr	Asp	Ser	Ala	Asn	Glu	Lys	Pro	Ala	Leu	Ile	Pro	Arg	170	175	180
Glu	Lys	Lys	Ile	Ser	Ile	Leu	Glu	Glu	Pro	Ser	Lys	Ala	Leu	Arg	185	190	195
Gly	Val	Thr	Glu	Gly	Asn	Arg	Leu	Leu	Gln	Gln	Lys	Leu	Ser	Leu	200	205	210
Asp	Gly	Asn	Pro	Lys	Pro	Ile	His	Gly	Thr	Thr	Glu	Arg	Ser	Asp	215	220	225
Gly	Leu	Gln	Trp	Ser	Ala	Glu	Gln	Pro	Cys	Asn	Pro	Ser	Lys	Pro	230	235	240
Lys	Ala	Lys	Thr	Ser	Pro	Val	Lys	Ser	Asn	Thr	Pro	Ala	Ala	His	245	250	255
Leu	Glu	Ile	Lys	Pro	Asp	Glu	Leu	Ala	Lys	Lys	Arg	Gly	Pro	Asn	260	265	270
Ile	Glu	Lys	Ser	Val	Lys	Asp	Leu	Gln	Arg	Cys	Thr	Val	Ser	Leu	275	280	285
Thr	Arg	Tyr	Arg	Val	Met	Ile	Lys	Glu	Glu	Val	Asp	Ser	Ser	Val	290	295	300
Lys	Lys	Ile	Lys	Ala	Ala	Phe	Ala	Glu	Leu	His	Asn	Cys	Ile	Ile	305	310	315
Asp	Lys	Glu	Val	Ser	Leu	Met	Ala	Glu	Met	Asp	Lys	Val	Lys	Glu	320	325	330
Glu	Ala	Met	Glu	Ile	Leu	Thr	Ala	Arg	Gln	Lys	Lys	Ala	Glu	Glu	335	340	345

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Leu	Lys	Arg	Leu	Thr	Asp	Leu	Ala	Ser	Gln	Met	Ala	Glu	Met	Gln
				350					355					360
Leu	Ala	Glu	Leu	Arg	Ala	Glu	Ile	Lys	His	Phe	Val	Ser	Glu	Arg
				365					370					375
Lys	Tyr	Asp	Glu	Glu	Leu	Gly	Lys	Ala	Ala	Arg	Phe	Ser	Cys	Asp
				380					385					390
Ile	Glu	Gln	Leu	Lys	Ala	Gln	Ile	Met	Leu	Cys	Gly	Glu	Ile	Thr
				395					400					405
His	Pro	Lys	Asn	Asn	Tyr	Ser	Ser	Arg	Thr	Pro	Cys	Ser	Ser	Leu
				410					415					420
Leu	Pro	Leu	Leu	Asn	Ala	His	Ala	Ala	Thr	Ser	Gly	Lys	Gln	Ser
				425					430					435
Asn	Phe	Ser	Arg	Lys	Ser	Ser	Thr	His	Asn	Lys	Pro	Ser	Glu	Gly
				440					445					450
Lys	Ala	Ala	Asn	Pro	Lys	Met	Val	Ser	Ser	Leu	Pro	Ser	Thr	Ala
				455					460					465
Asp	Pro	Ser	His	Gln	Thr	Met	Pro	Ala	Asn	Lys	Gln	Asn	Gly	Ser
				470					475					480
Ser	Asn	Gln	Arg	Arg	Arg	Phe	Asn	Pro	Gln	Tyr	His	Asn	Asn	Arg
				485					490					495
Leu	Asn	Gly	Pro	Ala	Lys	Ser	Gln	Gly	Ser	Gly	Asn	Glu	Ala	Glu
				500					505					510
Pro	Leu	Gly	Lys	Gly	Asn	Ser	Arg	His	Glu	His	Arg	Arg	Gln	Pro
				515					520					525
His	Asn	Gly	Phe	Arg	Pro	Lys	Asn	Lys	Gly	Gly	Ala	Lys	Asn	Gln
				530					535					540
Glu	Ala	Ser	Leu	Gly	Met	Lys	Thr	Pro	Glu	Ala	Pro	Ala	His	Ser
				545					550					555
Glu	Lys	Pro	Arg	Arg	Arg	Gln	His	Ala	Ala	Asp	Thr	Ser	Glu	Ala
				560					565					570
Arg	Pro	Phe	Arg	Gly	Ser	Val	Gly	Arg	Val	Ser	Gln	Cys	Asn	Leu
				575					580					585
Cys	Pro	Thr	Arg	Ile	Glu	Val	Ser	Thr	Asp	Ala	Ala	Val	Leu	Ser
				590					595					600
Val	Pro	Ala	Val	Thr	Leu	Val	Ala							
				605										

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: TESTTUT02
- (B) CLONE: 1273453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8 :

Met	Val	Ile	Ser	Trp	His	Leu	Ala	Ser	Asp	Met	Asp	Cys	Val	Val
				5					10					15
Thr	Leu	Thr	Thr	Asp	Ala	Ala	Arg	Arg	Ile	Tyr	Asp	Glu	Thr	Gln
				20					25					30
Gly	Arg	Gln	Gln	Val	Leu	Pro	Leu	Asp	Ser	Ile	Tyr	Lys	Lys	Thr
				35					40					45
Leu	Pro	Asp	Trp	Lys	Arg	Ser	Leu	Pro	His	Phe	Arg	Asn	Gly	Lys

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Leu	Tyr	Phe	Lys	Pro	Ile	Gly	Asp	Pro	Val	Phe	Ala	Arg	Asp	Leu	50	55	60
				65					70								75
Leu	Thr	Phe	Pro	Asp	Asn	Val	Glu	His	Cys	Glu	Thr	Val	Phe	Gly	80	85	90
Met	Leu	Leu	Gly	Asp	Thr	Ile	Ile	Leu	Asp	Asn	Leu	Asp	Ala	Ala	95	100	105
Asn	His	Tyr	Arg	Lys	Glu	Val	Val	Lys	Ile	Thr	His	Cys	Pro	Thr	110	115	120
Leu	Leu	Thr	Arg	Asp	Gly	Asp	Arg	Ile	Arg	Ser	Asn	Gly	Lys	Phe	125	130	135
Gly	Gly	Leu	Gln	Asn	Lys	Ala	Pro	Pro	Met	Asp	Lys	Leu	Arg	Gly	140	145	150
Met	Val	Phe	Gly	Ala	Pro	Val	Pro	Lys	Gln	Cys	Leu	Ile	Leu	Gly	155	160	165
Glu	Gln	Ile	Asp	Leu	Leu	Gln	Gln	Tyr	Arg	Ser	Ala	Val	Cys	Lys	170	175	180
Leu	Asp	Ser	Val	Asn	Lys	Asp	Leu	Asn	Ser	Gln	Leu	Glu	Tyr	Leu	185	190	195
Arg	Thr	Pro	Asp	Met	Arg	Lys	Lys	Lys	Gln	Glu	Leu	Asp	Glu	His	200	205	210
Glu	Lys	Asn	Leu	Lys	Leu	Ile	Glu	Glu	Lys	Leu	Gly	Met	Thr	Pro	215	220	225
Ile	Arg	Lys	Cys	Asn	Asp	Ser	Leu	Arg	His	Ser	Pro	Lys	Val	Glu	230	235	240
Thr	Thr	Asp	Cys	Pro	Val	Pro	Pro	Lys	Arg	Met	Arg	Arg	Glu	Ala	245	250	255
Thr	Arg	Gln	Asn	Arg	Ile	Ile	Thr	Lys	Thr	Asp	Val				260	265	

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: TESTTUT02
- (B) CLONE: 1275261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9 :

Met	Val	Met	Arg	Pro	Leu	Trp	Ser	Leu	Leu	Leu	Trp	Glu	Ala	Leu	5	10	15
Leu	Pro	Ile	Thr	Val	Thr	Gly	Ala	Gln	Val	Leu	Ser	Lys	Val	Gly	20	25	30
Gly	Ser	Val	Leu	Leu	Val	Ala	Ala	Arg	Pro	Pro	Gly	Phe	Gln	Val	35	40	45
Arg	Glu	Ala	Ile	Trp	Arg	Ser	Leu	Trp	Pro	Ser	Glu	Glu	Leu	Leu	50	55	60
Ala	Thr	Phe	Phe	Arg	Gly	Ser	Leu	Glu	Thr	Leu	Tyr	His	Ser	Arg	65	70	75
Phe	Leu	Gly	Arg	Ala	Gln	Leu	His	Ser	Asn	Leu	Ser	Leu	Glu	Leu	80	85	90
Gly	Pro	Leu	Glu	Ser	Gly	Asp	Ser	Gly	Asn	Phe	Ser	Val	Leu	Met	95	100	105

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Val	Asp	Thr	Arg	Gly	Gln	Pro	Trp	Thr	Gln	Thr	Leu	Gln	Leu	Lys
				110					115					120
Val	Tyr	Asp	Ala	Val	Pro	Arg	Pro	Val	Val	Gln	Val	Phe	Ile	Ala
				125					130					135
Val	Glu	Arg	Asp	Ala	Gln	Pro	Ser	Lys	Thr	Cys	Gln	Val	Phe	Leu
				140					145					150
Ser	Cys	Trp	Ala	Pro	Asn	Ile	Ser	Glu	Ile	Thr	Tyr	Ser	Trp	Arg
				155					160					165
Arg	Glu	Thr	Thr	Met	Asp	Phe	Gly	Met	Glu	Pro	His	Ser	Leu	Phe
				170					175					180
Thr	Asp	Gly	Gln	Val	Leu	Ser	Ile	Ser	Leu	Gly	Pro	Gly	Asp	Arg
				185					190					195
Asp	Val	Ala	Tyr	Ser	Cys	Ile	Val	Ser	Asn	Pro	Val	Ser	Trp	Asp
				200					205					210
Leu	Ala	Thr	Val	Thr	Pro	Trp	Asp	Ser	Cys	His	His	Glu	Ala	Ala
				215					220					225
Pro	Gly	Lys	Ala	Ser	Tyr	Lys	Asp	Val	Leu	Leu	Val	Val	Val	Pro
				230					235					240
Val	Ser	Leu	Leu	Leu	Met	Leu	Val	Thr	Leu	Phe	Ser	Ala	Trp	His
				245					250					255
Trp	Cys	Pro	Cys	Ser	Gly	Lys	Lys	Lys	Lys	Asp	Val	His	Ala	Asp
				260					265					270
Arg	Val	Gly	Pro	Glu	Thr	Glu	Asn	Pro	Leu	Val	Gln	Asp	Leu	Pro
				275					280					285

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNNOT16
- (B) CLONE: 1281682

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10 :

Met	Pro	Phe	Thr	Arg	Pro	Leu	Lys	His	Phe	Val	Ser	Leu	Leu	His
				5					10					15
Pro	Ser	Ala	Ser	Gln	Val	His	Asn	Ala	Gly	Gln	His	Gln	Lys	Leu
				20					25					30
Lys	Thr	Leu	Glu	Lys	Ala	Cys	Gly	Leu	Ala	Leu	Gly	Glu	Gly	Arg
				35					40					45
Glu	Gln	Asn	Leu	Cys	Thr	Ser	Leu	Phe	Asn	Leu	Glu	Ile	Arg	His
				50					55					60
Pro	Arg	Asp	Ala	Ile	Ile	Phe	Cys	Val	Ser	Ile	Val	Val	Pro	Leu
				65					70					75
Ser														

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

PF-0459 US

(A) LENGTH: 147 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: BRSTNOT07
(B) CLONE: 1298305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11 :

Met	Thr	Ala	Ser	Thr	Gly	His	Leu	Gly	Leu	Gly	Trp	Ser	Ala	Arg	
				5					10					15	
Pro	Cys	Pro	Cys	Gly	Thr	Leu	Gly	Ser	Cys	Phe	Leu	Ser	Leu	Phe	
				20					25					30	
Ala	Ala	Leu	Leu	Trp	Leu	Ala	Ala	Ala	Val	Leu	Gln	Ala	Cys	Val	
				35					40					45	
Gly	His	Ser	Asp	Glu	Gly	Cys	Gly	Ala	Ser	Gln	Cys	Arg	Arg	Ala	
				50					55					60	
Ala	Leu	Gly	Ile	Val	Pro	Ser	Pro	Val	Ser	Val	Leu	Arg	Thr	Tyr	
				65					70					75	
Pro	Gly	Leu	His	His	Gln	Asp	Pro	Val	Phe	Gly	Phe	Arg	Arg	Pro	
				80					85					90	
Ser	Met	Gly	Lys	Thr	Arg	His	Gln	Pro	Leu	Gln	Gln	Trp	Val	Pro	
				95					100					105	
Leu	Ala	Cys	Gly	His	Gln	Leu	Gly	Asp	Pro	Gly	Ser	Gly	Pro	Leu	
				110					115					120	
Leu	Ser	Pro	Val	Ser	Leu	Cys	Cys	Gly	Phe	Trp	Ala	Val	Met	Ser	
				125					130					135	
Pro	Pro	Leu	Lys	Asp	Val	Phe	Thr	Leu	Thr	Ser	Gly				
				140					145						

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 261 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: LUNGNOT12
(B) CLONE: 1360501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12 :

Met	Glu	Leu	Leu	Gln	Val	Thr	Ile	Leu	Phe	Leu	Leu	Pro	Ser	Ile	
				5					10					15	
Cys	Ser	Ser	Asn	Ser	Thr	Gly	Val	Leu	Glu	Ala	Ala	Asn	Asn	Ser	
				20					25					30	
Leu	Val	Val	Thr	Thr	Thr	Lys	Pro	Ser	Ile	Thr	Thr	Pro	Asn	Thr	
				35					40					45	
Glu	Ser	Leu	Gln	Lys	Asn	Val	Val	Thr	Pro	Thr	Thr	Gly	Thr	Thr	
				50					55					60	
Pro	Lys	Gly	Thr	Ile	Thr	Asn	Glu	Leu	Leu	Lys	Met	Ser	Leu	Met	
				65					70					75	
Ser	Thr	Ala	Thr	Phe	Leu	Thr	Ser	Lys	Asp	Glu	Gly	Leu	Lys	Ala	
				80					85					90	

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Thr	Thr	Thr	Asp	Val	Arg	Lys	Asn	Asp	Ser	Ile	Ile	Ser	Asn	Val
				95					100					105
Thr	Val	Thr	Ser	Val	Thr	Leu	Pro	Asn	Ala	Val	Ser	Thr	Leu	Gln
				110					115					120
Ser	Ser	Lys	Pro	Lys	Thr	Glu	Thr	Gln	Ser	Ser	Ile	Lys	Thr	Thr
				125					130					135
Glu	Ile	Pro	Gly	Ser	Val	Leu	Gln	Pro	Asp	Ala	Ser	Pro	Ser	Lys
				140					145					150
Thr	Gly	Thr	Leu	Thr	Ser	Ile	Pro	Val	Thr	Ile	Pro	Glu	Asn	Thr
				155					160					165
Ser	Gln	Ser	Gln	Val	Ile	Gly	Thr	Glu	Gly	Gly	Lys	Asn	Ala	Ser
				170					175					180
Thr	Ser	Ala	Thr	Ser	Arg	Ser	Tyr	Ser	Ser	Ile	Ile	Leu	Pro	Val
				185					190					195
Val	Ile	Ala	Leu	Ile	Val	Ile	Thr	Leu	Ser	Val	Phe	Val	Leu	Val
				200					205					210
Gly	Leu	Tyr	Arg	Met	Cys	Trp	Lys	Ala	Asp	Pro	Gly	Thr	Pro	Glu
				215					220					225
Asn	Gly	Asn	Asp	Gln	Pro	Gln	Ser	Asp	Lys	Glu	Ser	Val	Lys	Leu
				230					235					240
Leu	Thr	Val	Lys	Thr	Ile	Ser	His	Glu	Ser	Gly	Glu	His	Ser	Ala
				245					250					255
Gln	Gly	Lys	Thr	Lys	Asn									
				260										

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGNOT12
- (B) CLONE: 1362406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13 :

Met	Ala	Gly	Cys	Pro	Ala	Asp	Arg	Ser	Ile	Leu	Ala	Pro	Leu	Ala
				5					10					15
Trp	Asp	Leu	Gly	Leu	Leu	Leu	Phe	Val	Gly	Gln	His	Ser	Leu	
				20					25					30
Met	Ala	Ala	Glu	Arg	Val	Lys	Ala	Trp	Thr	Ser	Arg	Tyr	Phe	Gly
				35					40					45
Val	Leu	Gln	Arg	Ser	Leu	Tyr	Val	Ala	Cys	Thr	Ala	Leu	Ala	Leu
				50					55					60
Gln	Leu	Val	Met	Arg	Tyr	Trp	Glu	Pro	Ile	Pro	Lys	Gly	Pro	Val
				65					70					75
Leu	Trp	Glu	Ala	Arg	Ala	Glu	Pro	Trp	Ala	Thr	Trp	Val	Pro	Leu
				80					85					90
Leu	Cys	Phe	Val	Leu	His	Val	Ile	Ser	Trp	Leu	Leu	Ile	Phe	Ser
				95					100					105
Ile	Leu	Leu	Val	Phe	Asp	Tyr	Ala	Glu	Leu	Met	Gly	Leu	Lys	Gln
				110					115					120
Val	Tyr	Tyr	His	Val	Leu	Gly	Leu	Gly	Glu	Pro	Leu	Ala	Leu	Lys
				125					130					135
Ser	Pro	Arg	Ala	Leu	Arg	Leu	Phe	Ser	His	Leu	Arg	His	Pro	Val

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	140		145		150
Cys Val Glu Leu	Leu Thr Val Leu Trp	Val Val Pro Thr Leu	Gly		
	155		160		165
Thr Asp Arg Leu	Leu Leu Ala Phe Leu	Leu Thr Leu Tyr Leu	Gly		
	170		175		180
Leu Ala His Gly	Leu Asp Gln Gln Asp	Leu Arg Tyr Leu Arg	Ala		
	185		190		195
Gln Leu Gln Arg	Lys Leu His Leu Leu	Ser Arg Pro Gln Asp	Gly		
	200		205		210
Glu Ala Glu					

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LATRTUT02
- (B) CLONE: 1405329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14 :

Met Gln Pro Arg Pro Arg Gly Arg Pro Pro Arg Thr Arg Gly Asp		
	5	10
Glu Ala Pro Gln Trp His Leu Pro Asp Ala Ala Ala Leu Leu Pro		15
	20	25
Val Arg Leu Pro Leu Ala Val Leu Val Arg Gly Thr Gln Arg Pro		30
	35	40
Glu Arg Arg Arg Cys Gly Arg Leu Pro Ala Gly Val Pro Gly Ala		45
	50	55
Ala Arg Ser Val Ala Arg Ser		60
	65	

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAINOT12
- (B) CLONE: 1415223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15 :

Met Leu Ala Pro Gln Arg Thr Arg Ala Pro Ser Pro Arg Ala Ala		
	5	10
Pro Arg Pro Thr Arg Ser Met Leu Pro Ala Ala Met Lys Gly Leu		15
	20	25
		30

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Gly	Leu	Ala	Leu	Leu	Ala	Val	Leu	Leu	Cys	Ser	Ala	Pro	Ala	His	
			35						40					45	
Gly	Leu	Trp	Cys	Gln	Asp	Cys	Thr	Leu	Thr	Thr	Asn	Ser	Ser	His	
			50						55					60	
Cys	Thr	Pro	Lys	Gln	Cys	Gln	Pro	Ser	Asp	Thr	Val	Cys	Ala	Ser	
			65						70					75	
Val	Arg	Ile	Thr	Asp	Pro	Ser	Ser	Ser	Arg	Lys	Asp	His	Ser	Val	
			80						85					90	
Asn	Lys	Met	Cys	Ala	Ser	Ser	Cys	Asp	Phe	Val	Lys	Arg	His	Phe	
			95						100					105	
Phe	Ser	Asp	Tyr	Leu	Met	Gly	Phe	Ile	Asn	Ser	Gly	Ile	Leu	Lys	
			110						115					120	
Val	Asp	Val	Asp	Cys	Cys	Glu	Lys	Asp	Leu	Cys	Asn	Gly	Ala	Ala	
			125						130					135	
Gly	Ala	Gly	His	Ser	Pro	Trp	Ala	Leu	Ala	Gly	Gly	Leu	Leu	Leu	
			140						145					150	
Ser	Leu	Gly	Pro	Ala	Leu	Leu	Trp	Ala	Gly	Pro					
			155						160						

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAINOT12
- (B) CLONE: 1416553

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16 :

Met	Trp	Ala	Gln	Arg	Val	Leu	Thr	Leu	Trp	Gln	Gly	Leu	Ser	Trp	
				5					10					15	
Gly	Arg	Pro	Pro	Ser	Gly	Pro	Gly	Ala	Met	Ala	Pro	Arg	Gly	Gln	
				20					25					30	
Ala	Asp	Leu	Leu	Pro	Ala	Val	Ser	Thr	Pro	Phe	Leu	Ile	Thr	Val	
				35					40					45	
Trp	Ser	Pro	Ser	Phe	Gly	Cys	Ser	Leu	Arg	Cys	Val	Leu	Gly	Ser	
				50					55					60	
Ser	Glu	Pro	Glu	Ala	Ser	Phe	Trp	Lys	Pro	Ala	Val	Leu	Pro	Ala	
				65					70					75	
Pro	Val	Gln	Lys	Pro	Leu	Ser	Pro	Ala	Phe	Pro	Gln	Ala	Gly	Val	
				80					85					90	
Gly	Val	Gly	Gly	Leu	Cys	Pro	Ser	Ser	Leu	Thr	Leu	Glu	Arg	Trp	
				95					100					105	
Glu	Ala	Gly	Asn	Leu	His	Leu	Gly	Ala	Trp	Ala	Pro	Pro	Leu	Cys	
				110					115					120	
Ala	Ser	Gly	Phe	Pro	Ala	Pro	Gly	Arg	Gly	Cys	Ser	Pro	Ser	Trp	
				125					130					135	
Thr	Pro	Ala	Cys	Pro	Ser										
				140											

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 152 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
 (A) LIBRARY: KIDNNOT09
 (B) CLONE: 1418517

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17 :

Met	Glu	Asp	Glu	Glu	Val	Ala	Glu	Ser	Trp	Glu	Glu	Ala	Ala	Asp	
				5					10					15	
Ser	Gly	Glu	Ile	Asp	Arg	Arg	Leu	Glu	Lys	Lys	Leu	Lys	Ile	Thr	
				20					25					30	
Gln	Lys	Glu	Ser	Arg	Lys	Ser	Lys	Ser	Pro	Pro	Lys	Val	Pro	Ile	
				35					40					45	
Val	Ile	Gln	Asp	Asp	Ser	Leu	Pro	Ala	Gly	Pro	Pro	Pro	Gln	Ile	
				50					55					60	
Arg	Ile	Leu	Lys	Arg	Pro	Thr	Ser	Asn	Gly	Val	Val	Ser	Ser	Pro	
				65					70					75	
Asn	Ser	Thr	Ser	Arg	Pro	Thr	Leu	Pro	Val	Lys	Ser	Leu	Ala	Gln	
				80					85					90	
Arg	Glu	Ala	Glu	Tyr	Ala	Glu	Ala	Arg	Lys	Arg	Ile	Leu	Gly	Ser	
				95					100					105	
Ala	Ser	Pro	Glu	Glu	Glu	Gln	Glu	Lys	Pro	Ile	Leu	Asp	Arg	Pro	
				110					115					120	
Thr	Arg	Ile	Ser	Gln	Pro	Glu	Asp	Ser	Arg	Gln	Pro	Asn	Asn	Val	
				125					130					135	
Ile	Arg	Gln	Pro	Leu	Gly	Pro	Asp	Gly	Ser	Gln	Gly	Phe	Lys	Gln	
				140					145					150	
Arg	Arg														

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 742 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
 (A) LIBRARY: PANCNOT08
 (B) CLONE: 1438165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18 :

Met	Ala	Ser	Val	His	Glu	Ser	Leu	Tyr	Phe	Asn	Pro	Met	Met	Thr	
				5					10					15	
Asn	Gly	Val	Val	His	Ala	Asn	Val	Phe	Gly	Ile	Lys	Asp	Trp	Val	
				20					25					30	
Thr	Pro	Tyr	Lys	Ile	Ala	Val	Leu	Val	Leu	Leu	Asn	Glu	Met	Ser	
				35					40					45	
Arg	Thr	Gly	Glu	Gly	Ala	Val	Ser	Leu	Met	Glu	Arg	Arg	Arg	Leu	
				50					55					60	
Asn	Gln	Leu	Leu	Leu	Pro	Leu	Leu	Gln	Gly	Pro	Asp	Ile	Thr	Leu	

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Ser	Lys	Leu	Tyr	65	Leu	Ile	Glu	Glu	70	Ser	Cys	Pro	Gln	Leu	75	Ala
				80					85							90
Asn	Ser	Val	Gln	95	Arg	Ile	Lys	Leu	100	Met	Ala	Glu	Gly	Glu	Leu	105
Lys	Asp	Met	Glu	110	Phe	Phe	Asp	Asp	115	Leu	Ser	Asp	Ser	Phe	Ser	120
Gly	Thr	Glu	Pro	125	Val	His	Lys	Thr	130	Ser	Val	Val	Gly	Leu	Phe	135
Leu	Arg	His	Met	140	Ile	Leu	Ala	Tyr	145	Lys	Leu	Ser	Phe	Ser	Gln	150
Val	Phe	Lys	Leu	155	Tyr	Thr	Ala	Leu	160	Gln	Tyr	Phe	Gln	Asn	Gly	165
Glu	Lys	Lys	Thr	170	Val	Glu	Asp	Ala	175	Met	Glu	Leu	Thr	Ser	Arg	180
Asp	Glu	Gly	Glu	185	Arg	Lys	Met	Glu	190	Glu	Glu	Leu	Asp	Val	Ser	195
Val	Arg	Glu	Glu	200	Glu	Val	Ser	Cys	205	Gly	Pro	Leu	Ser	Gln	Lys	210
Gln	Ala	Glu	Phe	215	Phe	Leu	Ser	Gln	220	Ala	Ser	Leu	Leu	Lys	Asn	225
Asp	Glu	Thr	Lys	230	Ala	Leu	Thr	Pro	235	Ser	Leu	Gln	Lys	Glu	Leu	240
Asn	Asn	Leu	Leu	245	Lys	Phe	Asn	Pro	250	Phe	Ala	Glu	Ala	His	Tyr	255
Leu	Ser	Tyr	Leu	260	Asn	Asn	Leu	Arg	265	Gln	Asp	Val	Phe	Ser	Ser	270
Thr	His	Ser	Leu	275	Leu	His	Tyr	Phe	280	Arg	Leu	Ile	Leu	Thr	Gly	285
Ala	Glu	Ser	Lys	290	Ser	Asn	Gly	Glu	295	Gly	Tyr	Gly	Arg	Ser	Leu	300
Arg	Tyr	Ala	Ala	305	Leu	Asn	Leu	Ala	310	Leu	His	Cys	Arg	Phe	Gly	315
His	Tyr	Gln	Gln	320	Ala	Glu	Leu	Ala	325	Gln	Glu	Ala	Ile	Arg	Ile	330
Ala	Gln	Glu	Ser	335	Asn	Asp	His	Val	340	Leu	Gln	His	Cys	Leu	Ser	345
Trp	Leu	Tyr	Val	350	Leu	Gly	Gln	Lys	355	Ser	Asp	Ser	Tyr	Val	Leu	360
Leu	Glu	His	Ser	365	Val	Lys	Lys	Ala	370	His	Phe	Gly	Leu	Pro	Arg	375
Ala	Phe	Ala	Gly	380	Lys	Thr	Ala	Asn	385	Leu	Met	Asp	Ala	Leu	Lys	390
Asp	Ser	Asp	Leu	395	Leu	His	Trp	Lys	400	Ser	Leu	Ser	Glu	Leu	Ile	405
Asp	Ile	Ser	Ile	410	Ala	Gln	Lys	Thr	415	Ile	Trp	Arg	Leu	Tyr	Gly	420
Arg	Ser	Thr	Met	425	Ala	Leu	Gln	Gln	430	Gln	Met	Leu	Leu	Ser	Met	435
Asn	Ser	Leu	Glu	440	Ala	Val	Asn	Ala	445	Val	Gln	Gln	Asn	Asn	Thr	450
Glu	Ser	Phe	Ala	455	Val	Ala	Leu	Cys	460	Leu	Ala	Glu	Leu	His	Ala	465
Glu	Gln	Gly	Cys	470	Phe	Ala	Ala	Ala	475	Glu	Val	Leu	Lys	His	Leu	480
Lys	Glu	Arg	Phe	485	Pro	Pro	Asn	Ser	490	His	Ala	Gln	Leu	Trp	Met	495
Leu	Cys	Asp	Gln	500	Lys	Ile	Gln	Phe	505	Arg	Ala	Met	Asn	Asp	Gly	510
Lys	Tyr	His	Leu	515	Ala	Asp	Ser	Leu	520	Thr	Gly	Ile	Thr	Ala	Leu	525

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Asn	Ser	Ile	Glu	Gly	Val	Tyr	Arg	Lys	Ala	Val	Val	Leu	Gln	Ala	
				530					535					540	
Gln	Asn	Gln	Met	Ser	Glu	Ala	His	Lys	Leu	Leu	Gln	Lys	Leu	Leu	
				545					550					555	
Val	His	Cys	Gln	Lys	Leu	Lys	Asn	Thr	Glu	Met	Val	Ile	Ser	Val	
				560					565					570	
Leu	Leu	Ser	Val	Ala	Glu	Leu	Tyr	Trp	Arg	Ser	Ser	Ser	Pro	Thr	
				575					580					585	
Ile	Ala	Leu	Pro	Met	Leu	Leu	Gln	Ala	Leu	Ala	Leu	Ser	Lys	Glu	
				590					595					600	
Tyr	Arg	Leu	Gln	Tyr	Leu	Ala	Ser	Glu	Thr	Val	Leu	Asn	Leu	Ala	
				605					610					615	
Phe	Ala	Gln	Leu	Ile	Leu	Gly	Ile	Pro	Glu	Gln	Ala	Leu	Ser	Leu	
				620					625					630	
Leu	His	Met	Ala	Ile	Glu	Pro	Ile	Leu	Ala	Asp	Gly	Ala	Ile	Leu	
				635					640					645	
Asp	Lys	Gly	Arg	Ala	Met	Phe	Leu	Val	Ala	Lys	Cys	Gln	Val	Ala	
				650					655					660	
Ser	Ala	Ala	Ser	Tyr	Asp	Gln	Pro	Lys	Lys	Ala	Glu	Ala	Leu	Glu	
				665					670					675	
Ala	Ala	Ile	Glu	Asn	Leu	Asn	Glu	Ala	Lys	Asn	Tyr	Phe	Ala	Lys	
				680					685					690	
Val	Asp	Cys	Lys	Glu	Arg	Ile	Arg	Asp	Val	Val	Tyr	Phe	Gln	Ala	
				695					700					705	
Arg	Leu	Tyr	His	Thr	Leu	Gly	Lys	Thr	Gln	Glu	Arg	Asn	Arg	Cys	
				710					715					720	
Ala	Met	Leu	Phe	Arg	Gln	Leu	His	Gln	Glu	Leu	Pro	Ser	His	Gly	
				725					730					735	
Val	Pro	Leu	Ile	Asn	His	Leu									
				740											

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THYRNOT03
- (B) CLONE: 1440381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19 :

Met	Asp	Gly	Ile	Leu	Asp	Glu	Ser	Leu	Leu	Glu	Thr	Cys	Pro	Ile	
				5					10					15	
Gln	Ser	Pro	Leu	Gln	Val	Phe	Ala	Gly	Met	Gly	Gly	Leu	Ala	Leu	
				20					25					30	
Ile	Ala	Glu	Arg	Leu	Pro	Met	Leu	Tyr	Pro	Glu	Val	Ile	Gln	Gln	
				35					40					45	
Val	Ser	Ala	Pro	Val	Val	Thr	Ser	Thr	Thr	Gln	Glu	Lys	Pro	Tyr	
				50					55					60	
Asp	Ser	Asp	Gln	Phe	Glu	Trp	Val	Thr	Ile	Glu	Gln	Ser	Gly	Glu	
				65					70					75	
Leu	Val	Tyr	Glu	Ala	Pro	Glu	Thr	Val	Ala	Ala	Glu	Pro	Pro	Pro	
				80					85					90	
Ile	Lys	Ser	Ala	Val	Gln	Thr	Met	Ser	Pro	Ile	Pro	Ala	His	Ser	

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Leu	Ala	Ala	Phe	95	Leu	Phe	Leu	Arg	100	Leu	Pro	Gly	Tyr	Ala	105	Glu
				110					115							120
Val	Leu	Leu	Lys	125	Arg	Lys	His	Ala	130	Gln	Cys	Leu	Leu	Arg	135	Leu
Val	Leu	Gly	Val	140	Thr	Asp	Asp	Gly	145	Gly	Ser	His	Ile	Leu	150	Gln
Ser	Pro	Ser	Ala	155	Asn	Val	Leu	Pro	160	Leu	Pro	Phe	His	Val	165	Leu
Arg	Ser	Leu	Phe	170	Ser	Thr	Thr	Pro	175	Leu	Thr	Asp	Asp	Gly	180	Val
Leu	Leu	Arg	Arg	185	Met	Ala	Leu	Glu	190	Gly	Ala	Leu	His	Leu	195	Ile
Leu	Val	Cys	Leu	200	Ser	Ala	Leu	Ser	205	His	Ser	Pro	Arg	Val	210	Pro
Asn	Ser	Ser	Val	215	Asn	Gln	Thr	Glu	220	Gln	Val	Ser	Ser	Ser	225	His
Asn	Pro	Thr	Ser	230	Thr	Glu	Glu	Gln	235	Leu	Tyr	Trp	Ala	Lys	240	Gly
Thr	Gly	Phe	Gly	245	Thr	Gly	Ser	Thr	250	Ser	Gly	Trp	Asp	Val	255	Glu
Gln	Ala	Leu	Thr	260	Lys	Gln	Arg	Leu	265	Glu	Glu	His	Val	Thr	270	Cys
Leu	Leu	Gln	Val	275	Leu	Ala	Ser	Tyr	280	Asn	Pro	Val	Ser	Ser	285	Ala
Val	Asn	Gly	Glu	290	Ala	Gln	Ser	Ser	295	Glu	Thr	Arg	Gly	Gln	300	Asn
Ser	Asn	Ala	Leu	305	Pro	Ser	Val	Leu	310	Glu	Leu	Leu	Ser	Gln	315	Ser
Cys	Leu	Ile	Pro	320	Ala	Met	Ser	Ser	325	Leu	Arg	Asn	Asp	Ser	330	Val
Leu	Asp	Met	Ala	335	Arg	His	Val	Pro	340	Leu	Tyr	Arg	Ala	Leu	345	Glu
Leu	Leu	Arg	Ala	350	Ile	Ala	Ser	Cys	355	Ala	Met	Val	Pro	Leu	360	Leu
Leu	Pro	Leu	Ser	365	Thr	Glu	Asn	Gly	370	Glu	Glu	Glu	Glu	Gln	375	Ser
Glu	Cys	Gln	Thr	380	Ser	Val	Gly	Thr	385	Leu	Ala	Lys	Met	Lys	390	Thr
Cys	Val	Asp	Thr	395	Tyr	Thr	Asn	Arg	400	Arg	Ser	Lys	Arg	Glu	405	Asn
Val	Lys	Thr	Gly	410	Val	Lys	Pro	Asp	415	Ser	Asp	Gln	Glu	Pro	420	Glu
Gly	Leu	Thr	Leu	425	Leu	Val	Pro	Asp	430	Gln	Lys	Thr	Ala	Glu	435	Ile
Val	Tyr	Ala	Ala	440	Thr	Thr	Ser	Leu	445	Gln	Ala	Asn	Gln	Glu	450	Lys
Asn	Trp	Val	Asn	455	Thr	Pro	Arg	Arg	460	Leu	Met	Asn	Pro	Lys	465	Pro
Leu	Ser	Val	Leu	470	Lys	Ser	Leu	Glu	475	Glu	Tyr	Val	Ala	Val	480	Met
Lys	Lys	Leu	Gln	485	Phe	Asp	Thr	Phe	490	Met	Val	Ser	Glu	Asp	495	Glu
Asp	Gly	Lys	Leu	500	Gly	Phe	Lys	Val	505	Tyr	His	Tyr	Met	Ser	510	Gln
Val	Lys	Asn	Ala	515	Asn	Asp	Ala	Asn	520	Ala	Ala	Arg	Ala	Arg	525	Arg
Leu	Ala	Gln	Glu	530	Ala	Val	Thr	Leu	535	Thr	Ser	Leu	Pro	Leu	540	Ser
Ser	Ser	Ser	Ser	545	Val	Phe	Val	Arg	550	Asp	Glu	Glu	Arg	Leu	555	Asp

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Ile Met Lys Val	Leu	Ile Thr Gly Pro	Ala	Asp Thr Pro Tyr	Ala
	560		565		570
Asn Gly Cys Phe	Glu Phe Asp Val Tyr	Phe	Pro Gln Asp Tyr	Pro	
	575		580		585
Ser Ser Pro Pro	Leu Val Asn Leu Glu	Thr Thr Gly Gly His	Ser		
	590		595		600
Val Arg Phe Asn	Pro Asn Leu Tyr Asn	Asp Gly Lys Val Cys	Leu		
	605		610		615
Ser Ile Leu Asn	Thr Trp His Gly Arg	Pro Glu Glu Lys Trp	Asn		
	620		625		630
Pro Gln Thr Ser	Ser Phe Leu Gln Val	Leu Val Ser Val Gln	Ser		
	635		640		645
Leu Ile Leu Val	Ala Glu Pro Tyr Phe	Asn Glu Pro Gly Tyr	Glu		
	650		655		660
Arg Ser Arg Gly	Thr Pro Ser Gly Thr	Gln Ser Ser Arg Glu	Tyr		
	665		670		675
Asp Gly Asn Ile	Arg Gln Ala Thr Val	Lys Trp Ala Met Leu	Glu		
	680		685		690
Gln Ile Arg Asn	Pro Ser Pro Cys Phe	Lys Glu Val Ile His	Lys		
	695		700		705
His Phe Tyr Leu	Lys Arg Val Glu Ile	Met Ala Gln Cys Glu	Glu		
	710		715		720
Trp Ile Ala Asp	Ile Gln Gln Tyr Ser	Ser Asp Lys Arg Val	Gly		
	725		730		735
Arg Thr Met Ser	His His Ala Ala Ala	Leu Lys Arg His Thr	Ala		
	740		745		750
Gln Leu Arg Glu	Glu Leu Leu Lys Leu	Pro Cys Pro Glu Gly	Leu		
	755		760		765
Asp Pro Asp Thr	Asp Asp Ala Pro Glu	Val Cys Arg Ala Thr	Thr		
	770		775		780
Gly Ala Glu Glu	Thr Leu Met His Asp	Gln Val Lys Pro Ser	Ser		
	785		790		795
Ser Lys Glu Leu	Pro Ser Asp Phe Gln	Leu			
	800		805		

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGNOT14
- (B) CLONE: 1510839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20 :

Met Lys Ala Ser Gln Cys Cys Cys Cys	Leu	Ser His Leu Leu	Ala
	5		15
Ser Val Leu Leu Leu Leu Leu Leu Pro	Glu	Leu Ser Gly Pro	Leu
	20		30
Ala Val Leu Leu Gln Ala Ala Glu Ala	Ala	Pro Gly Leu Gly	Pro
	35		45
Pro Asp Pro Arg Pro Arg Thr Leu Pro	Pro	Leu Pro Pro Gly	Pro
	50		60
Thr Pro Ala Gln Gln Pro Gly Arg Gly	Leu	Ala Glu Ala Ala	Gly

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Pro	Arg	Gly	Ser	65	Glu	Gly	Gly	Asn	Gly	70	Ser	Asn	Pro	Val	Ala	Gly	75
				80						85							90
Leu	Glu	Thr	Asp	95	Asp	His	Gly	Gly	Lys	100	Ala	Gly	Glu	Gly	Ser	Val	105
Gly	Gly	Gly	Leu	110	Ala	Val	Ser	Pro	Asn	115	Pro	Gly	Asp	Lys	Pro	Met	120
Thr	Gln	Arg	Ala	125	Leu	Thr	Val	Leu	Met	130	Val	Val	Ser	Gly	Ala	Val	135
Leu	Val	Tyr	Phe	140	Val	Val	Arg	Thr	Val	145	Arg	Met	Arg	Arg	Arg	Asn	150
Arg	Lys	Thr	Arg	155	Arg	Tyr	Gly	Val	Leu	160	Asp	Thr	Asn	Ile	Glu	Asn	165
Met	Glu	Leu	Thr	170	Pro	Leu	Glu	Gln	Asp	175	Asp	Glu	Asp	Asp	Asp	Asn	180
Thr	Leu	Phe	Asp	185	Ala	Asn	His	Pro	Arg	190	Arg	Arg	Glu	Cys	Ala	Phe	195

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SPLNNOT04
- (B) CLONE: 1534876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21 :

Met	Trp	Phe	Leu	Gly	Cys	Thr	Gly	Pro	Gly	Cys	Gly	Cys	Ala	Gly			
				5					10					15			
Val	Cys	Lys	Val	20	Val	Pro	Cys	Ile	Ser	Thr	Gly	Phe	Glu	Thr	Ser		
				25										30			
Gly	Pro	Cys	Pro	35	Ser	Ser	Arg	Glu	Gly	Phe	Leu	Phe	Phe	Leu	Thr		
				40										45			
Gln	Val	Thr	Phe	50	Gln	Pro	Phe	Gln	Phe	Pro	Ser	Phe	Ser	Ala	Leu		
				55										60			
Pro	Ser	Asn	Ser	65	Ala	Asn	Pro	Gly	Val	Gly	Ser	Gln	Gly	Gly	Arg		
				70										75			
Glu	Cys	Pro	Thr	80	Thr	Phe	Ser	Gly	Gln	Pro	Leu	Thr	Pro	Lys	Pro		
				85										90			
Leu	Pro	Pro	Ser	95	Ile	Leu	His	Pro	Leu	Pro	Ile	Gln	Pro	Lys	Cys		
				100										105			
Pro	Gln	Leu	Gly	110	Leu	Ser	Cys	Ile	Pro	Val	Glu	Gly	Pro	Leu	Pro		
				115										120			
Cys	Leu	Ser	Glu	125	Val	Arg	Leu	Cys	Cys	Val	Met	Gly	Arg	Leu	Cys		
				130										135			
Pro	Ser	Pro	Pro	140	Leu	Ala	Arg	Cys	Thr	Cys	Phe	Leu	Val	Cys	Thr		
				145										150			
Arg	Cys	Pro	Gly	155	Gly	Pro	Ser	Leu	Pro	Cys	Gln						
				160													

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SPLNNOT04
- (B) CLONE: 1559131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22 :

Met	Asp	Lys	Leu	Lys	Lys	Val	Leu	Ser	Gly	Gln	Asp	Thr	Glu	Asp	5	10	15
Arg	Ser	Gly	Leu	Ser	Glu	Val	Val	Glu	Ala	Ser	Ser	Leu	Ser	Trp	20	25	30
Ser	Thr	Arg	Ile	Lys	Gly	Phe	Ile	Ala	Cys	Phe	Ala	Ile	Gly	Ile	35	40	45
Leu	Cys	Ser	Leu	Leu	Gly	Thr	Val	Leu	Leu	Trp	Val	Pro	Arg	Lys	50	55	60
Gly	Leu	His	Leu	Phe	Ala	Val	Phe	Tyr	Thr	Phe	Gly	Asn	Ile	Ala	65	70	75
Ser	Ile	Gly	Ser	Thr	Ile	Phe	Leu	Met	Gly	Pro	Val	Lys	Gln	Leu	80	85	90
Lys	Arg	Met	Phe	Glu	Pro	Thr	Arg	Leu	Ile	Ala	Thr	Ile	Met	Val	95	100	105
Leu	Leu	Cys	Phe	Ala	Leu	Thr	Leu	Cys	Ser	Ala	Phe	Trp	Trp	His	110	115	120
Asn	Lys	Gly	Leu	Ala	Leu	Ile	Phe	Cys	Ile	Leu	Gln	Ser	Leu	Ala	125	130	135
Leu	Thr	Trp	Tyr	Ser	Leu	Ser	Phe	Ile	Pro	Phe	Ala	Arg	Asp	Ala	140	145	150
Val	Lys	Lys	Cys	Phe	Ala	Val	Cys	Leu	Ala						155	160	

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BLADNOT03
- (B) CLONE: 1601473

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23 :

Met	Gln	Ala	Lys	Tyr	Ser	Ser	Thr	Arg	Asp	Met	Leu	Asp	Asp	Asp	5	10	15
Gly	Asp	Thr	Thr	Met	Ser	Leu	His	Ser	Gln	Ala	Ser	Ala	Thr	Thr	20	25	30
Arg	His	Pro	Glu	Pro	Arg	Arg	Thr	Glu	His	Arg	Ala	Pro	Ser	Ser	35	40	45
Thr	Trp	Arg	Pro	Val	Ala	Leu	Thr	Leu	Leu	Thr	Leu	Cys	Leu	Val	50	55	60

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Leu Leu Ile Gly Leu Ala Ala Leu Gly Leu Leu Cys Lys Ser Ala
65 70 75
Leu

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 336 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: BRAITUT12

(B) CLONE: 1615809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24 :

Met Ile Ser Tyr Ile Val Leu Leu Ser Ile Leu Leu Trp Pro Leu
5 10 15
Val Val Tyr His Glu Leu Ile Gln Arg Met Tyr Thr Arg Leu Glu
20 25 30
Pro Leu Leu Met Gln Leu Asp Tyr Ser Met Lys Ala Glu Ala Asn
35 40 45
Ala Leu His His Lys His Asp Lys Arg Lys Arg Gln Gly Lys Asn
50 55 60
Ala Pro Pro Gly Gly Asp Glu Pro Leu Ala Glu Thr Glu Ser Glu
65 70 75
Ser Glu Ala Glu Leu Ala Gly Phe Ser Pro Val Val Asp Val Lys
80 85 90
Lys Thr Ala Leu Ala Leu Ala Ile Thr Asp Ser Glu Leu Ser Asp
95 100 105
Glu Glu Ala Ser Ile Leu Glu Ser Gly Gly Phe Ser Val Ser Arg
110 115 120
Ala Thr Thr Pro Gln Leu Thr Asp Val Ser Glu Asp Leu Asp Gln
125 130 135
Gln Ser Leu Pro Ser Glu Pro Glu Glu Thr Leu Ser Arg Asp Leu
140 145 150
Gly Glu Gly Glu Glu Gly Glu Leu Ala Pro Pro Glu Asp Leu Leu
155 160 165
Gly Arg Pro Gln Ala Leu Ser Arg Gln Ala Leu Asp Ser Glu Glu
170 175 180
Glu Glu Glu Asp Val Ala Ala Lys Glu Thr Leu Leu Arg Leu Ser
185 190 195
Ser Pro Leu His Phe Val Asn Thr His Phe Asn Gly Ala Gly Ser
200 205 210
Pro Gln Asp Gly Val Lys Cys Ser Pro Gly Gly Pro Val Glu Thr
215 220 225
Leu Ser Pro Glu Thr Val Ser Gly Gly Leu Thr Ala Leu Pro Gly
230 235 240
Thr Leu Ser Pro Pro Leu Cys Leu Val Gly Ser Asp Pro Ala Pro
245 250 255
Ser Pro Ser Ile Leu Pro Pro Val Pro Gln Asp Ser Pro Gln Pro
260 265 270
Leu Pro Ala Pro Glu Glu Glu Glu Ala Leu Thr Thr Glu Asp Phe
275 280 285
Glu Leu Leu Asp Gln Gly Glu Leu Glu Gln Leu Asn Ala Glu Leu
290 295 300
Gly Leu Glu Pro Glu Thr Pro Pro Lys Pro Pro Asp Ala Pro Pro
305 310 315
Leu Gly Pro Asp Ile His Ser Leu Val Gln Ser Asp Gln Glu Ala

Gln Ala Val Ala Glu Pro 320 325 330
335

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNNOT19
- (B) CLONE: 1634813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25 :

Met	Asn	Leu	Trp	Leu	Leu	Ala	Cys	Leu	Val	Ala	Gly	Phe	Leu	Gly	5	10	15
Ala	Trp	Ala	Pro	Ala	Val	His	Ala	Gln	Gly	Val	Phe	Glu	Asp	Cys	20	25	30
Cys	Leu	Ala	Tyr	His	Tyr	Pro	Ile	Gly	Trp	Ala	Val	Leu	Arg	Arg	35	40	45
Ala	Trp	Thr	Tyr	Arg	Ile	Gln	Glu	Val	Ser	Gly	Ser	Cys	Asn	Leu	50	55	60
Pro	Ala	Ala	Ile	Phe	Tyr	Leu	Pro	Lys	Arg	His	Arg	Lys	Val	Cys	65	70	75
Gly	Asn	Pro	Lys	Ser	Arg	Glu	Val	Gln	Arg	Ala	Met	Lys	Leu	Leu	80	85	90
Asp	Ala	Arg	Asn	Lys	Val	Phe	Ala	Lys	Leu	Arg	His	Asn	Thr	Gln	95	100	105
Thr	Phe	Gln	Ala	Gly	Pro	His	Ala	Val	Lys	Lys	Leu	Ser	Ser	Gly	110	115	120
Asn	Ser	Lys	Leu	Ser	Ser	Ser	Lys	Phe	Ser	Asn	Pro	Ile	Ser	Ser	125	130	135
Ser	Lys	Arg	Asn	Val	Ser	Leu	Leu	Ile	Ser	Ala	Asn	Ser	Gly	Leu	140	145	150

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: UTRSNOT06
- (B) CLONE: 1638407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26 :

Met	Ala	Pro	Pro	Ala	Leu	Gln	Arg	Gly	Gln	Arg	Val	Ala	Ala	Val	5	10	15
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Ala	Val	Gly	Ser	Gln	Ala	Val	Leu	Gln	Ile	Leu	Ser	Arg	Val	Ser	
				20					25					30	
Gly	Arg	Gln	Ala	Pro	Pro	Gln	Pro	Ser	Gly	Ser	Gly	Gly	Val	Gly	
				35					40					45	
Ala	Gly	Pro	Val	Val	Val	Pro	Asp	Gly	Gly	Gly	Glu	Gly	Pro	Gln	
				50					55					60	
Pro	His	Pro	Ser	Ser	Ser	Gln	Ser	Pro	Pro	Asp	Leu	Pro	Leu	Lys	
				65					70					75	
Ala	Gly	Asp	Thr	Val	Met	Gly	Lys	Gln	Ala	Gln	Arg	Asp	Ile	Arg	
				80					85					90	
Leu	Arg	Val	Arg	Ala	Glu	Tyr	Cys	Glu	His	Gly	Pro	Ala	Leu	Glu	
				95					100					105	
Gln	Gly	Val	Ala	Ser	Arg	Arg	Pro	Gln	Ala	Leu	Ala	Arg	Gln	Leu	
				110					115					120	
Asp	Val	Phe	Gly	Gln	Ala	Thr	Ala	Val	Leu	Arg	Ser	Arg	Asp	Leu	
				125					130					135	
Gly	Ser	Val	Val	Cys	Asp	Ile	Lys	Phe	Ser	Glu	Leu	Ser	Tyr	Leu	
				140					145					150	
Asp	Ala	Phe	Trp	Gly	Asp	Tyr	Leu	Ser	Gly	Ala	Leu	Leu	Gln	Ala	
				155					160					165	
Leu	Arg	Gly	Val	Phe	Leu	Thr	Glu	Ala	Leu	Arg	Glu	Ala	Val	Gly	
				170					175					180	
Arg	Glu	Ala	Val	Arg	Leu	Leu	Val	Ser	Val	Asp	Glu	Ala	Asp	Tyr	
				185					190					195	
Glu	Ala	Gly	Arg	Arg	Arg	Leu	Leu	Leu	Met	Ala	Glu	Glu	Gly	Gly	
				200					205					210	
Arg	Arg	Pro	Thr	Glu	Ala	Ser									
				215											

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 504 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: PROSTUT08

(B) CLONE: 1653112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27 :

Met	Ser	Gln	Pro	Arg	Thr	Pro	Glu	Gln	Ala	Leu	Asp	Thr	Pro	Gly	
				5					10					15	
Asp	Cys	Pro	Pro	Gly	Arg	Arg	Asp	Glu	Asp	Ala	Gly	Glu	Gly	Ile	
				20					25					30	
Gln	Cys	Ser	Gln	Arg	Met	Leu	Ser	Phe	Ser	Asp	Ala	Leu	Leu	Ser	
				35					40					45	
Ile	Ile	Ala	Thr	Val	Met	Ile	Leu	Pro	Val	Thr	His	Thr	Glu	Ile	
				50					55					60	
Ser	Pro	Glu	Gln	Gln	Phe	Asp	Arg	Ser	Val	Gln	Arg	Leu	Leu	Ala	
				65					70					75	
Thr	Arg	Ile	Ala	Val	Tyr	Leu	Met	Thr	Phe	Leu	Ile	Val	Thr	Val	
				80					85					90	
Ala	Trp	Ala	Ala	His	Thr	Arg	Leu	Phe	Gln	Val	Val	Gly	Lys	Thr	
				95					100					105	
Asp	Asp	Thr	Leu	Ala	Leu	Leu	Asn	Leu	Ala	Cys	Met	Met	Thr	Ile	

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Thr Phe Leu Pro	110	Thr Phe Ser Leu	115	Val Thr Phe Pro	120
Tyr	125	Met	130	Asp	135
Val Pro Leu Gly	140	Phe Leu Phe Cys	145	Val Cys Val Ile Ala	150
Gly Val Val Gln	155	Ala Leu Ile Val Gly	160	Tyr Ala Phe His Phe	165
His Leu Leu Ser	170	Pro Gln Ile Gln Arg	175	Ser Ala His Arg Ala	180
Tyr Arg Arg His	185	Val Leu Gly Ile Val	190	Leu Gln Gly Pro Ala	195
Cys Phe Ala Ala	200	Ala Ile Phe Ser Leu	205	Phe Phe Val Pro Leu	210
Tyr Leu Leu Met	215	Val Thr Val Ile Leu	220	Leu Pro Tyr Val Ser	225
Val Thr Gly Trp	230	Cys Arg Asp Arg Leu	235	Leu Gly His Arg Glu	240
Ser Ala His Pro	245	Val Glu Val Phe Ser	250	Phe Asp Leu His Glu	255
Leu Ser Lys Glu	260	Arg Val Glu Ala Phe	265	Ser Asp Gly Val Tyr	270
Ile Val Ala Thr	275	Leu Leu Ile Leu Asp	280	Ile Cys Glu Asp Asn	285
Pro Asp Pro Lys	290	Asp Val Lys Glu Arg	295	Phe Ser Gly Ser Leu	300
Ala Ala Leu Ser	305	Ala Thr Gly Pro Arg	310	Phe Leu Ala Tyr Phe	315
Ser Phe Ala Thr	320	Val Gly Leu Leu Trp	325	Phe Ala His His Ser	330
Phe Leu His Val	335	Arg Lys Ala Thr Arg	340	Ala Met Gly Leu Leu	345
Thr Leu Ser Leu	350	Ala Phe Val Gly Gly	355	Leu Pro Leu Ala Tyr	360
Gln Thr Ser Ala	365	Phe Ala Arg Gln Pro	370	Arg Asp Glu Leu Glu	375
Val Arg Val Ser	380	Cys Thr Ile Ile Phe	385	Leu Ala Ser Ile Phe	390
Leu Ala Met Trp	395	Thr Thr Ala Leu Leu	400	His Gln Ala Glu Thr	405
Gln Pro Ser Val	410	Trp Phe Gly Gly Arg	415	Glu His Val Leu Met	420
Ala Lys Leu Ala	425	Leu Tyr Pro Cys Ala	430	Ser Leu Leu Ala Phe	435
Ser Thr Cys Leu	440	Leu Ser Arg Phe Ser	445	Val Gly Ile Phe His	450
Met Gln Ile Ala	455	Val Pro Cys Ala Phe	460	Leu Leu Leu Arg Leu	465
Val Gly Leu Ala	470	Leu Ala Thr Leu Arg	475	Val Leu Arg Gly Leu	480
Arg Pro Glu His	485	Pro Pro Pro Ala Pro	490	Thr Gly Gln Asp Asp	495
Gln Ser Gln Leu	500	Leu Pro Ala Pro Cys			

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 320 amino acids

PF-0459 US

(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: BRSTNOT09
(B) CLONE: 1664634

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28 :

Met	Ala	Ala	Arg	Leu	Asp	Gly	Gly	Phe	Ala	Ala	Val	Ser	Arg	Ala	
				5					10					15	
Phe	His	Glu	Ile	Arg	Ala	Arg	Asn	Pro	Ala	Phe	Gln	Pro	Gln	Thr	
				20					25					30	
Leu	Met	Asp	Phe	Gly	Ser	Gly	Thr	Gly	Ser	Val	Thr	Trp	Ala	Ala	
				35					40					45	
His	Ser	Ile	Trp	Gly	Gln	Ser	Leu	Arg	Glu	Tyr	Met	Cys	Val	Asp	
				50					55					60	
Arg	Ser	Ala	Ala	Met	Leu	Val	Leu	Ala	Glu	Lys	Leu	Leu	Thr	Gly	
				65					70					75	
Gly	Ser	Glu	Ser	Gly	Glu	Pro	Tyr	Ile	Pro	Gly	Val	Phe	Phe	Arg	
				80					85					90	
Gln	Phe	Leu	Pro	Val	Ser	Pro	Lys	Val	Gln	Phe	Asp	Val	Val	Val	
				95					100					105	
Ser	Ala	Phe	Ser	Leu	Ser	Asp	Gln	Leu	Leu	Thr	Phe	Ile	Leu	Ser	
				110					115					120	
Cys	Asn	Ser	Ser	Leu	Leu	His	Ile	Phe	Pro	Phe	Cys	Glu	Gln	Val	
				125					130					135	
Leu	Val	Glu	Asn	Gly	Thr	Lys	Ala	Gly	His	Ser	Leu	Leu	Met	Asp	
				140					145					150	
Ala	Arg	Asp	Leu	Val	Leu	Lys	Gly	Lys	Glu	Lys	Ser	Pro	Leu	Asp	
				155					160					165	
Pro	Arg	Pro	Gly	Phe	Val	Phe	Ala	Pro	Cys	Pro	His	Glu	Leu	Pro	
				170					175					180	
Cys	Pro	Gln	Leu	Thr	Asn	Leu	Ala	Cys	Ser	Phe	Ser	Gln	Ala	Tyr	
				185					190					195	
His	Pro	Ile	Pro	Phe	Ser	Trp	Asn	Lys	Lys	Pro	Lys	Glu	Glu	Lys	
				200					205					210	
Phe	Ser	Met	Val	Ile	Leu	Ala	Arg	Gly	Ser	Pro	Glu	Glu	Ala	His	
				215					220					225	
Arg	Trp	Pro	Arg	Ile	Thr	Gln	Pro	Val	Leu	Lys	Arg	Pro	Arg	His	
				230					235					240	
Val	His	Cys	His	Leu	Cys	Cys	Pro	Asp	Gly	His	Met	Gln	His	Ala	
				245					250					255	
Val	Leu	Thr	Ala	Arg	Arg	His	Gly	Arg	Tyr	Gly	Gly	Cys	Asp	Gln	
				260					265					270	
Asn	Gln	Trp	Asp	Val	Ala	Gly	Ser	Cys	Ser	Pro	Arg	Gln	His	Leu	
				275					280					285	
Phe	Pro	Gln	Gly	Phe	Val	Ser	Leu	Cys	Pro	Cys	Gln	Leu	Leu	Gly	
				290					295					300	
Arg	Ser	Phe	Thr	Cys	Ala	Tyr	Ser	Val	Cys	Val	Ser	Ser	Ile	Tyr	
				305					310					315	
Gly	Ser	Gly	Ser	Leu											
				320											

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

PF-0459 US

(A) LENGTH: 117 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: PROSTUT10
(B) CLONE: 1690990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29 :

Met	Asp	Asn	Lys	Gly	Ile	Tyr	Pro	Gly	Ala	Val	Phe	Tyr	His	Asp	
				5					10					15	
Ser	Phe	Thr	Glu	Ser	Arg	Val	Val	Leu	Leu	Arg	Ile	Arg	Thr	Leu	
			20						25					30	
Val	Pro	Tyr	Ser	Pro	Pro	Asp	Cys	Pro	Thr	Thr	Thr	Thr	Ala	Tyr	
			35						40					45	
Ser	Pro	Phe	Pro	Asn	His	Gly	Gln	Gln	Ile	Glu	Leu	Leu	Thr	Glu	
			50						55					60	
Val	Ser	Phe	Arg	Trp	Ile	Ser	Gln	Pro	Phe	Pro	His	Arg	Pro	His	
			65						70					75	
Arg	Glu	Thr	Val	Thr	Asp	Cys	Tyr	Ser	Pro	Asn	Thr	Gln	Val	Lys	
			80						85					90	
Ser	Asn	Ala	Gly	Arg	Asn	Asn	Ser	Lys	Ser	Phe	Asn	Phe	Leu	Ile	
			95						100					105	
Leu	Leu	Leu	Lys	Ile	Leu	Thr	Glu	Ala	Ser	Arg	Phe				
			110						115						

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 298 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: DUODNOT02
(B) CLONE: 1704050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30 :

Met	Ala	Arg	Arg	Ser	Arg	His	Arg	Leu	Leu	Leu	Leu	Leu	Leu	Arg	
				5					10					15	
Tyr	Leu	Val	Val	Ala	Leu	Gly	Tyr	His	Lys	Ala	Tyr	Gly	Phe	Ser	
			20						25					30	
Ala	Pro	Lys	Asp	Gln	Gln	Val	Val	Thr	Ala	Val	Glu	Tyr	Gln	Glu	
			35						40					45	
Ala	Ile	Leu	Ala	Cys	Lys	Thr	Pro	Lys	Lys	Thr	Val	Ser	Ser	Arg	
			50						55					60	
Leu	Glu	Trp	Lys	Lys	Leu	Gly	Arg	Ser	Val	Ser	Phe	Val	Tyr	Tyr	
			65						70					75	
Gln	Gln	Thr	Leu	Gln	Gly	Asp	Phe	Lys	Asn	Arg	Ala	Glu	Met	Ile	
			80						85					90	
Asp	Phe	Asn	Ile	Arg	Ile	Lys	Asn	Val	Thr	Arg	Ser	Asp	Ala	Gly	
			95						100					105	
Lys	Tyr	Arg	Cys	Glu	Val	Ser	Ala	Pro	Ser	Glu	Gln	Gly	Gln	Asn	
			110						115					120	

[illegible]

(2) INFORMATION FOR SEQ ID NO: 31:

(A) LENGTH: 118 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) LIBRARY: PROSNOT16
(B) CLONE: 1711840

Met	Gln	His	Arg	Gly	Phe	Leu	Leu	Leu	Thr	Leu	Leu	Ala	Leu	Leu
				5					10					15
Ala	Leu	Thr	Ser	Ala	Val	Ala	Lys	Lys	Gln	Asp	Lys	Val	Lys	Lys
				20					25					30
Gly	Gly	Pro	Gly	Ser	Glu	Cys	Ala	Glu	Trp	Ala	Trp	Gly	Pro	Cys
				35					40					45
Thr	Pro	Ser	Ser	Lys	Gly	Phe	Ala	Ala	Val	Gly	Phe	Pro	Arg	Gly
				50					55					60
Pro	Pro	Trp	Gly	Gly	Pro	Arg	Thr	Gln	Pro	Ala	Val	Leu	Val	Glu
				65					70					75
Arg	Val	Ala	Pro	Gly	Lys	Leu	Glu	Arg	Lys	Glu	Phe	Trp	Ala	Pro
				80					85					90
Gly	Leu	Trp	Lys	Val	Gly	Gln	Ile	Phe	Trp	Lys	Lys	Thr	Trp	Arg
				95					100					105
Val	Cys	Arg	Ser	Val	Lys	Trp	Gly	Arg	Gly	Gln	Lys	Asn		
				110					115					

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32 :

Met	Gln	Thr	Cys	Pro	Leu	Ala	Phe	Pro	Gly	His	Val	Ser	Gln	Ala	5	10	15
Leu	Gly	Thr	Leu	Leu	Phe	Leu	Ala	Ala	Ser	Leu	Ser	Ala	Gln	Asn	20	25	30
Glu	Gly	Trp	Asp	Ser	Pro	Ile	Cys	Thr	Glu	Gly	Val	Val	Ser	Val	35	40	45
Ser	Trp	Gly	Glu	Asn	Thr	Val	Met	Ser	Cys	Asn	Ile	Ser	Asn	Ala	50	55	60
Phe	Ser	His	Val	Asn	Ile	Lys	Leu	Arg	Ala	His	Gly	Gln	Glu	Ser	65	70	75
Ala	Ile	Phe	Asn	Glu	Val	Ala	Pro	Gly	Tyr	Phe	Ser	Arg	Asp	Gly	80	85	90
Trp	Gln	Leu	Gln	Val	Gln	Gly	Gly	Val	Ala	Gln	Leu	Val	Ile	Lys	95	100	105
Gly	Ala	Arg	Asp	Ser	His	Ala	Gly	Leu	Tyr	Met	Trp	His	Leu	Val	110	115	120
Gly	His	Gln	Arg	Asn	Asn	Arg	Gln	Val	Thr	Leu	Glu	Val	Ser	Gly	125	130	135
Ala	Glu	Pro	Gln	Ser	Ala	Pro	Asp	Thr	Gly	Phe	Trp	Pro	Val	Pro	140	145	150
Ala	Val	Val	Thr	Ala	Val	Phe	Ile	Leu	Leu	Val	Ala	Leu	Val	Met	155	160	165
Phe	Ala	Trp	Tyr	Arg	Cys	Arg	Cys	Ser	Gln	Gln	Arg	Arg	Glu	Lys	170	175	180
Lys	Phe	Phe	Leu	Leu	Glu	Pro	Gln	Met	Lys	Val	Ala	Ala	Leu	Arg	185	190	195
Ala	Gly	Ala	Gln	Gln	Gly	Leu	Ser	Arg	Ala	Ser	Ala	Glu	Leu	Trp	200	205	210
Thr	Pro	Asp	Ser	Glu	Pro	Thr	Pro	Arg	Pro	Leu	Ala	Leu	Val	Phe	215	220	225
Lys	Pro	Ser	Pro	Leu	Gly	Ala	Leu	Glu	Leu	Leu	Ser	Pro	Gln	Pro	230	235	240
Leu	Phe	Pro	Tyr	Ala	Ala	Asp	Pro								245		

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: STOMTUT02

(B) CLONE: 1750632

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33 :

Met	Leu	Glu	Glu	Gly	Ser	Phe	Arg	Gly	Arg	Thr	Ala	Asp	Phe	Val	5	10	15
Phe	Met	Phe	Leu	Phe	Gly	Gly	Val	Leu	Met	Thr	Val	Ser	Phe	Pro	20	25	30
Gln	Ala	Leu	Glu	Pro	Arg	Ala	Arg	Ala	Pro	Arg	Arg	Pro	Ala	Cys	35	40	45
Val	Gly	Pro	Gly	Ala	Asn	Thr	Ala	Met	Pro	Glu	Arg	Asp	Thr	Val	50	55	60
Ala	Val	Ser	Ser	Leu	Ala	Pro	Phe	Leu	Pro	Trp	Ala	Leu	Met	Gly	65	70	75
Phe	Ser	Leu	Leu	Leu	Gly	Asn	Ser	Ile	Leu	Val	Asp	Leu	Leu	Gly	80	85	90
Ile	Ala	Val	Gly	His	Ile	Tyr	Tyr	Phe	Leu	Glu	Asp	Val	Phe	Pro	95	100	105
Asn	Gln	Pro	Gly	Gly	Lys	Arg	Leu	Leu	Gln	Thr	Pro	Gly	Phe	Leu	110	115	120
Lys	Leu	Leu	Leu	Asp	Ala	Pro	Ala	Glu	Asp	Pro	Asn	Tyr	Leu	Pro	125	130	135
Leu	Pro	Glu	Glu	Gln	Pro	Gly	Pro	His	Leu	Pro	Pro	Pro	Gln	Gln	140	145	150

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 431 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34 :

Met	Trp	Ala	Leu	Gly	Gln	Ala	Gly	Phe	Ala	Asn	Leu	Thr	Glu	Gly	5	10	15
Leu	Lys	Val	Trp	Leu	Gly	Ile	Met	Leu	Pro	Val	Leu	Gly	Ile	Lys	20	25	30
Ser	Leu	Ser	Pro	Phe	Ala	Ile	Thr	Tyr	Leu	Asp	Arg	Leu	Leu	Leu	35	40	45
Met	His	Pro	Asn	Leu	Thr	Lys	Gly	Phe	Gly	Met	Ile	Gly	Pro	Lys	50	55	60
Asp	Phe	Phe	Pro	Leu	Leu	Asp	Phe	Ala	Tyr	Met	Pro	Asn	Asn	Ser	65	70	75
Leu	Thr	Pro	Ser	Leu	Gln	Glu	Gln	Leu	Cys	Gln	Leu	Tyr	Pro	Arg	80	85	90
Leu	Lys	Met	Leu	Ala	Phe	Gly	Ala	Lys	Pro	Asp	Ser	Thr	Leu	His	95	100	105
Thr	Tyr	Phe	Pro	Ser	Phe	Leu	Ser	Arg	Ala	Thr	Pro	Ser	Cys	Pro	110	115	120

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Pro	Glu	Met	Lys	Lys	Glu	Leu	Leu	Ser	Ser	Leu	Thr	Glu	Cys	Leu	125	130	135
Thr	Val	Asp	Pro	Leu	Ser	Ala	Ser	Val	Trp	Arg	Gln	Leu	Tyr	Pro	140	145	150
Lys	His	Leu	Ser	Gln	Ser	Ser	Leu	Leu	Leu	Glu	His	Leu	Leu	Ser	155	160	165
Ser	Trp	Glu	Gln	Ile	Pro	Lys	Lys	Val	Gln	Lys	Ser	Leu	Gln	Glu	170	175	180
Thr	Ile	Gln	Ser	Leu	Lys	Leu	Thr	Asn	Gln	Glu	Leu	Leu	Arg	Lys	185	190	195
Gly	Ser	Ser	Asn	Asn	Gln	Asp	Val	Val	Thr	Cys	Asp	Met	Ala	Cys	200	205	210
Lys	Gly	Leu	Leu	Gln	Gln	Val	Gln	Gly	Pro	Arg	Leu	Pro	Trp	Thr	215	220	225
Arg	Leu	Leu	Leu	Leu	Leu	Leu	Val	Phe	Ala	Val	Gly	Phe	Leu	Cys	230	235	240
His	Asp	Leu	Arg	Ser	His	Ser	Ser	Phe	Gln	Ala	Ser	Leu	Thr	Gly	245	250	255
Arg	Leu	Leu	Arg	Ser	Ser	Gly	Phe	Leu	Pro	Ala	Ser	Gln	Gln	Ala	260	265	270
Cys	Ala	Lys	Leu	Tyr	Ser	Tyr	Ser	Leu	Gln	Gly	Tyr	Ser	Trp	Leu	275	280	285
Gly	Glu	Thr	Leu	Pro	Leu	Trp	Gly	Ser	His	Leu	Leu	Thr	Val	Val	290	295	300
Arg	Pro	Ser	Leu	Gln	Leu	Ala	Trp	Ala	His	Thr	Asn	Ala	Thr	Val	305	310	315
Ser	Phe	Leu	Ser	Ala	His	Cys	Ala	Ser	His	Leu	Ala	Trp	Phe	Gly	320	325	330
Asp	Ser	Leu	Thr	Ser	Leu	Ser	Gln	Arg	Leu	Gln	Ile	Gln	Leu	Pro	335	340	345
Asp	Ser	Val	Asn	Gln	Leu	Leu	Arg	Tyr	Leu	Arg	Glu	Leu	Pro	Leu	350	355	360
Leu	Phe	His	Gln	Asn	Val	Leu	Leu	Pro	Leu	Trp	His	Leu	Leu	Leu	365	370	375
Glu	Ala	Leu	Ala	Trp	Ala	Gln	Glu	His	Cys	His	Glu	Ala	Cys	Arg	380	385	390
Gly	Glu	Val	Thr	Trp	Asp	Cys	Met	Lys	Thr	Gln	Leu	Ser	Glu	Ala	395	400	405
Val	His	Trp	Thr	Trp	Leu	Cys	Leu	Gln	Asp	Ile	Thr	Val	Ala	Phe	410	415	420
Leu	Asp	Trp	Ala	Leu	Ala	Leu	Ile	Ser	Gln	Gln					425	430	

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNOT20
- (B) CLONE: 1818761

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35 :

Met	Gln	Trp	Leu	Arg	Val	Arg	Glu	Ser	Pro	Gly	Glu	Ala	Thr	Gly	5	10	15
His	Arg	Val	Thr	Met	Gly	Thr	Ala	Ala	Leu	Gly	Pro	Val	Trp	Ala	20	25	30
Ala	Leu	Leu	Leu	Phe	Leu	Leu	Met	Cys	Glu	Ile	Pro	Met	Val	Glu	35	40	45
Leu	Thr	Phe	Asp	Arg	Ala	Val	Ala	Ser	Gly	Cys	Gln	Arg	Cys	Cys	50	55	60
Asp	Ser	Glu	Asp	Pro	Leu	Asp	Pro	Ala	His	Val	Ser	Ser	Ala	Ser	65	70	75
Ser	Ser	Gly	Arg	Pro	His	Ala	Leu	Pro	Glu	Ile	Arg	Pro	Tyr	Ile	80	85	90
Asn	Ile	Thr	Ile	Leu	Lys	Gly	Asp	Lys	Gly	Asp	Pro	Gly	Pro	Met	95	100	105
Gly	Leu	Pro	Gly	Tyr	Met	Gly	Arg	Glu	Gly	Pro	Gln	Gly	Glu	Pro	110	115	120
Gly	Pro	Gln	Gly	Ser	Lys	Gly	Asp	Lys	Gly	Glu	Met	Gly	Ser	Pro	125	130	135
Gly	Ala	Pro	Cys	Gln	Lys	Arg	Phe	Phe	Ala	Phe	Ser	Val	Gly	Arg	140	145	150
Lys	Thr	Ala	Leu	His	Ser	Gly	Glu	Asp	Phe	Gln	Thr	Leu	Leu	Phe	155	160	165
Glu	Arg	Val	Phe	Val	Asn	Leu	Asp	Gly	Cys	Phe	Asp	Met	Ala	Thr	170	175	180
Gly	Gln	Phe	Ala	Ala	Pro	Leu	Arg	Gly	Ile	Tyr	Phe	Phe	Ser	Leu	185	190	195
Asn	Val	His	Ser	Trp	Asn	Tyr	Lys	Glu	Thr	Tyr	Val	His	Ile	Met	200	205	210
His	Asn	Gln	Lys	Glu	Ala	Val	Ile	Leu	Tyr	Ala	Gln	Pro	Ser	Glu	215	220	225
Arg	Ser	Ile	Met	Gln	Ser	Gln	Ser	Val	Met	Leu	Asp	Leu	Ala	Tyr	230	235	240
Gly	Asp	Arg	Val	Trp	Val	Arg	Leu	Phe	Lys	Arg	Gln	Arg	Glu	Asn	245	250	255
Ala	Ile	Tyr	Ser	Asn	Asp	Phe	Asp	Thr	Tyr	Ile	Thr	Phe	Ser	Gly	260	265	270
His	Leu	Ile	Lys	Ala	Glu	Asp	Asp								275		

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GBLATUT01
- (B) CLONE: 1824469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36 :

Met	Glu	Glu	Lys	Arg	Arg	Arg	Ala	Arg	Val	Gln	Gly	Ala	Trp	Ala	5	10	15
Ala	Pro	Val	Lys	Ser	Gln	Ala	Ile	Ala	Gln	Pro	Ala	Thr	Thr	Ala			

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				20					25					30
Lys	Ser	His	Leu	His	Gln	Lys	Pro	Gly	Gln	Thr	Trp	Lys	Asn	Lys
				35					40					45
Glu	His	His	Leu	Ser	Asp	Arg	Glu	Phe	Val	Phe	Lys	Glu	Pro	Gln
				50					55					60
Gln	Val	Val	Arg	Arg	Ala	Pro	Glu	Pro	Arg	Val	Ile	Asp	Arg	Glu
				65					70					75
Gly	Val	Tyr	Glu	Ile	Ser	Leu	Ser	Pro	Thr	Gly	Val	Ser	Arg	Val
				80					85					90
Cys	Leu	Tyr	Pro	Gly	Phe	Val	Asp	Val	Lys	Glu	Ala	Asp	Trp	Ile
				95					100					105
Leu	Glu	Gln	Leu	Cys	Gln	Asp	Val	Pro	Trp	Lys	Gln	Arg	Thr	Gly
				110					115					120
Ile	Arg	Glu	Asp	Ile	Thr	Tyr	Gln	Gln	Pro	Arg	Leu	Thr	Ala	Trp
				125					130					135
Tyr	Gly	Glu	Leu	Pro	Tyr	Thr	Tyr	Ser	Arg	Ile	Thr	Met	Glu	Pro
				140					145					150
Asn	Pro	His	Trp	His	Pro	Val	Leu	Arg	Thr	Leu	Lys	Asn	Arg	Ile
				155					160					165
Glu	Glu	Asn	Thr	Gly	His	Thr	Phe	Asn	Ser	Leu	Leu	Cys	Asn	Leu
				170					175					180
Tyr	Arg	Asn	Glu	Lys	Asp	Ser	Val	Asp	Trp	His	Ser	Asp	Asp	Glu
				185					190					195
Pro	Ser	Leu	Gly	Arg	Cys	Pro	Ile	Ile	Ala	Ser	Leu	Ser	Phe	Gly
				200					205					210
Ala	Thr	Arg	Thr	Phe	Glu	Met	Arg	Lys	Lys	Pro	Pro	Pro	Glu	Glu
				215					220					225
Asn	Gly	Asp	Tyr	Thr	Tyr	Val	Glu	Arg	Val	Lys	Ile	Pro	Leu	Asp
				230					235					240
His	Gly	Thr	Leu	Leu	Ile	Met	Glu	Gly	Ala	Thr	Gln	Ala	Asp	Trp
				245					250					255
Gln	His	Arg	Val	Pro	Lys	Glu	Tyr	His	Ser	Arg	Glu	Pro	Arg	Val
				260					265					270
Asn	Leu	Thr	Phe	Arg	Thr	Val	Tyr	Pro	Asp	Pro	Arg	Gly	Ala	Pro
				275					280					285
Trp														

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNOT19
- (B) CLONE: 1864292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37 :

Met	Lys	Met	Glu	Glu	Ala	Val	Gly	Lys	Val	Glu	Glu	Leu	Ile	Glu
				5					10					15
Ser	Glu	Ala	Pro	Pro	Lys	Ala	Ser	Glu	Gln	Glu	Thr	Ala	Lys	Glu
				20					25					30
Glu	Asp	Gly	Ser	Val	Glu	Leu	Glu	Ser	Gln	Val	Gln	Lys	Asp	Gly
				35					40					45

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Val	Ala	Asp	Ser	Thr	Val	Ile	Ser	Ser	Met	Pro	Cys	Leu	Leu	Met
				50					55					60
Glu	Leu	Arg	Arg	Asp	Ser	Ser	Glu	Ser	Gln	Leu	Ala	Ser	Thr	Glu
				65					70					75
Ser	Asp	Lys	Pro	Thr	Thr	Gly	Arg	Val	Tyr	Glu	Ser	Asp	Pro	Ser
				80					85					90
Asn	His	Cys	Met	Leu	Ser	Pro	Ser	Ser	Ser	Gly	His	Leu	Ala	Asp
				95					100					105
Ser	Asp	Thr	Leu	Ser	Ser	Ala	Glu	Glu	Asn	Glu	Pro	Ser	Gln	Ala
				110					115					120
Glu	Thr	Ala	Val	Glu	Gly	Asp	Pro	Ser	Gly	Val	Ser	Gly	Ala	Thr
				125					130					135
Val	Gly	Arg	Lys	Ser	Arg	Arg	Ser	Arg	Ser	Glu	Ser	Glu	Thr	Ser
				140					145					150
Thr	Met	Ala	Ala	Lys	Lys	Asn	Arg	Gln	Ser	Ser	Asp	Lys	Gln	Asn
				155					160					165
Gly	Arg	Val	Ala	Lys	Val	Lys	Gly	His	Arg	Ser	Gln	Lys	His	Lys
				170					175					180
Glu	Arg	Ile	Arg	Leu	Leu	Arg	Gln	Lys	Arg	Glu	Ala	Ala	Ala	Arg
				185					190					195
Lys	Lys	Tyr	Asn	Leu	Leu	Gln	Asp	Ser	Ser	Thr	Ser	Asp	Ser	Asp
				200					205					210
Leu	Thr	Cys	Asp	Ser	Ser	Thr	Ser	Ser	Ser	Asp	Asp	Asp	Glu	Glu
				215					220					225
Val	Ser	Gly	Ser	Ser	Lys	Thr	Ile	Thr	Ala	Glu	Ile	Pro	Asp	Gly
				230					235					240
Pro	Pro	Val	Val	Ala	His	Tyr	Asp	Met	Ser	Asp	Thr	Asn	Ser	Asp
				245					250					255
Pro	Glu	Val	Val	Asn	Val	Asp	Asn	Leu	Leu	Ala	Ala	Ala	Val	Val
				260					265					270
Gln	Glu	His	Ser	Asn	Ser	Val	Gly	Gly	Gln	Asp	Thr	Gly	Ala	Thr
				275					280					285
Trp	Arg	Thr	Ser	Gly	Leu	Leu	Glu	Glu	Leu	Asn	Ala	Glu	Ala	Gly
				290					295					300
His	Leu	Asp	Pro	Gly	Phe	Leu	Ala	Ser	Asp	Lys	Thr	Ser	Ala	Gly
				305					310					315
Asn	Ala	Pro	Leu	Asn	Glu	Glu	Ile	Asn	Ile	Ala	Ser	Ser	Asp	Ser
				320					325					330
Glu	Val	Glu	Ile	Val	Gly	Val	Gln	Glu	His	Ala	Arg	Cys	Val	His
				335					340					345
Pro	Arg	Gly	Gly	Val	Ile	Gln	Ser	Val	Ser	Ser	Trp	Lys	His	Gly
				350					355					360
Ser	Gly	Thr	Gln	Tyr	Val	Ser	Thr	Arg	Gln	Thr	Gln	Ser	Trp	Thr
				365					370					375
Ala	Val	Thr	Pro	Gln	Gln	Thr	Trp	Ala	Ser	Pro	Ala	Glu	Val	Val
				380					385					390
Asp	Leu	Thr	Leu	Asp	Glu	Asp	Ser	Arg	Arg	Lys	Tyr	Leu	Leu	
				395					400					

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

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(A) LIBRARY: THP1NOT01

(B) CLONE: 1866437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38 :

Met	Phe	Val	Gln	Glu	Glu	Lys	Ile	Phe	Ala	Gly	Lys	Val	Leu	Arg	
				5					10					15	
Leu	His	Ile	Cys	Ala	Ser	Asp	Gly	Ala	Glu	Trp	Leu	Glu	Glu	Ala	
				20					25					30	
Thr	Glu	Asp	Thr	Ser	Val	Glu	Lys	Leu	Lys	Glu	Arg	Cys	Leu	Lys	
				35					40					45	
His	Cys	Ala	His	Gly	Ser	Leu	Glu	Asp	Pro	Lys	Ser	Ile	Thr	His	
				50					55					60	
His	Lys	Leu	Ile	His	Ala	Ala	Ser	Glu	Arg	Val	Leu	Ser	Asp	Ala	
				65					70					75	
Arg	Thr	Ile	Leu	Glu	Glu	Asn	Ile	Gln	Asp	Gln	Asp	Val	Leu	Leu	
				80					85					90	
Leu	Lys	Lys	Lys	Arg	Ala	Pro	Ser	Pro	Leu	Pro	Lys	Met	Ala	Asp	
				95					100					105	
Val	Ser	Ala	Glu	Glu	Lys	Lys	Lys	Gln	Asp	Gln	Lys	Ala	Pro	Asp	
				110					115					120	
Lys	Glu	Ala	Ile	Leu	Arg	Ala	Thr	Ala	Asn	Leu	Pro	Ser	Tyr	Asn	
				125					130					135	
Met	Asp	Arg	Ala	Ala	Val	Gln	Thr	Asn	Met	Arg	Asp	Phe	Gln	Thr	
				140					145					150	
Glu	Leu	Arg	Lys	Ile	Leu	Val	Ser	Leu	Ile	Glu	Val	Ala	Gln	Lys	
				155					160					165	
Leu	Leu	Ala	Leu	Asn	Pro	Asp	Ala	Val	Glu	Leu	Phe	Lys	Lys	Ala	
				170					175					180	
Asn	Ala	Met	Leu	Asp	Glu	Asp	Glu	Asp	Glu	Arg	Val	Asp	Glu	Ala	
				185					190					195	
Ala	Leu	Arg	Gln	Leu	Thr	Glu	Met	Gly	Phe	Pro	Glu	Asn	Arg	Ala	
				200					205					210	
Thr	Lys	Ala	Leu	Gln	Leu	Asn	His	Met	Ser	Val	Pro	Gln	Ala	Met	
				215					220					225	
Glu	Trp	Leu	Ile	Glu	His	Ala	Glu	Asp	Pro	Thr	Ile	Asp	Thr	Pro	
				230					235					240	
Leu	Pro	Gly	Gln	Ala	Pro	Pro	Glu	Ala	Glu	Gly	Ala	Thr	Ala	Ala	
				245					250					255	
Ala	Ser	Glu	Ala	Ala	Ala	Gly	Ala	Ser	Ala	Thr	Asp	Glu	Glu	Ala	
				260					265					270	
Arg	Asp	Glu	Leu	Thr	Glu	Ile	Phe	Lys	Lys	Ile	Arg	Arg	Lys	Arg	
				275					280					285	
Glu	Phe	Arg	Ala	Asp	Ala	Arg	Ala	Val	Ile	Ser	Leu	Met	Glu	Met	
				290					295					300	
Gly	Phe	Asp	Glu	Lys	Glu	Val	Ile	Asp	Ala	Leu	Arg	Val	Asn	Asn	
				305					310					315	
Asn	Gln	Gln	Asn	Ala	Ala	Cys	Glu	Trp	Leu	Leu	Gly	Asp	Arg	Lys	
				320					325					330	
Pro	Ser	Pro	Glu	Glu	Leu	Asp	Lys	Gly	Ile	Asp	Pro	Asp	Ser	Pro	
				335					340					345	
Leu	Phe	Gln	Ala	Ile	Leu	Asp	Asn	Pro	Val	Val	Gln	Leu	Gly	Leu	
				350					355					360	
Thr	Asn	Pro	Lys	Thr	Leu	Leu	Ala	Phe	Glu	Asp	Met	Leu	Glu	Asn	
				365					370					375	
Pro	Leu	Asn	Ser	Thr	Gln	Trp	Met	Asn	Asp	Pro	Glu	Thr	Gly	Pro	
				380					385					390	
Val	Met	Leu	Gln	Ile	Ser	Arg	Ile	Phe	Gln	Thr	Leu	Asn	Arg	Thr	
				395					400					405	

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SKINBIT01
- (B) CLONE: 1871375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39 :

Met	Val	Met	His	Asn	Ser	Asp	Pro	Asn	Leu	His	Leu	Leu	Ala	Glu	5	10	15
Gly	Ala	Pro	Ile	Asp	Trp	Gly	Glu	Glu	Tyr	Ser	Asn	Ser	Gly	Gly	20	25	30
Gly	Gly	Ser	Pro	Ala	Pro	Ala	Pro	Arg	Ser	Gln	Pro	Pro	Ser	Arg	35	40	45
Lys	Ser	Asp	Gly	Ala	Pro	Ser	Arg	Trp	Ser	Leu	Trp	Ser	Arg	Met	50	55	60
Arg	Arg	Trp	Gly	Cys	Pro	Leu	Arg	Leu	Ala	Leu	Ser	His	His	His	65	70	75
Leu	Arg	Pro	Arg	Thr	Val	Ser	Leu	Arg	Ser	Glu	Ala	Cys	Trp	Pro	80	85	90
Lys	Val	Cys	Gly	Leu	Arg	Ala	Pro	His	Gln	Pro	Ala	Pro	Cys	Ser	95	100	105
Thr	Gly	Pro	Pro	Leu	Gly	Arg	Val	Pro	Ser	Leu	Arg	Pro	Pro	Pro	110	115	120
Arg	Pro	Pro	Arg	Arg	Leu	Pro	His	Pro	Ser	Ser	Ile	Ser	Cys	Leu	125	130	135
Glu	Arg	Leu	Trp	Thr	Leu	Gly	Pro	Pro	Ser	Pro	Ala	Thr	Arg	Arg	140	145	150
Leu	Glu	Ser	Arg	Cys	Pro	Ala	Pro	Ala	Ala	Thr	Pro	Pro	Ser	Thr	155	160	165
Pro	Pro	Pro	Arg	Xaa	Xaa	Phe	Lys	Gly	Cys	Lys	Asn				170	175	

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LEUKNOT03
- (B) CLONE: 1880830

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40 :

Met	Ile	Thr	Cys	Arg	Val	Cys	Gln	Ser	Leu	Ile	Asn	Val	Glu	Gly	5	10	15
Lys	Met	His	Gln	His	Val	Val	Lys	Cys	Gly	Val	Cys	Asn	Glu	Ala	20	25	30

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Thr	Pro	Ile	Lys	Asn	Ala	Pro	Pro	Gly	Lys	Lys	Tyr	Val	Arg	Cys	
				35					40					45	
Pro	Cys	Asn	Cys	Leu	Leu	Ile	Cys	Lys	Val	Thr	Ser	Gln	Arg	Ile	
				50					55					60	
Ala	Cys	Pro	Arg	Pro	Tyr	Cys	Lys	Arg	Ile	Ile	Asn	Leu	Gly	Pro	
				65					70					75	
Val	His	Pro	Gly	Pro	Leu	Ser	Pro	Glu	Pro	Gln	Pro	Met	Gly	Val	
				80					85					90	
Arg	Val	Ile	Cys	Gly	His	Cys	Lys	Asn	Thr	Phe	Leu	Trp	Thr	Glu	
				95					100					105	
Phe	Thr	Asp	Arg	Thr	Leu	Ala	Arg	Cys	Pro	His	Cys	Arg	Lys	Val	
				110					115					120	
Ser	Ser	Ile	Gly	Arg	Arg	Tyr	Pro	Arg	Lys	Arg	Cys	Ile	Cys	Cys	
				125					130					135	
Phe	Leu	Leu	Gly	Leu	Leu	Leu	Ala	Val	Thr	Ala	Thr	Gly	Leu	Ala	
				140					145					150	
Phe	Gly	Thr	Trp	Lys	His	Ala	Arg	Arg	Tyr	Gly	Gly	Ile	Tyr	Ala	
				155					160					165	
Ala	Trp	Ala	Phe	Val	Ile	Leu	Leu	Ala	Val	Leu	Cys	Leu	Gly	Arg	
				170					175					180	
Ala	Leu	Tyr	Trp	Ala	Cys	Met	Lys	Val	Ser	His	Pro	Val	Gln	Asn	
				185					190					195	
Phe	Ser														

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: OVARNOT07
- (B) CLONE: 1905325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41 :

Met	Leu	Lys	Asp	Ile	Ile	Lys	Glu	Tyr	Thr	Asp	Val	Tyr	Pro	Glu	
				5					10					15	
Ile	Ile	Glu	Arg	Ala	Gly	Tyr	Ser	Leu	Glu	Lys	Val	Phe	Gly	Ile	
				20					25					30	
Gln	Leu	Lys	Glu	Ile	Asp	Lys	Asn	Asp	His	Leu	Tyr	Ile	Leu	Leu	
				35					40					45	
Ser	Thr	Leu	Glu	Pro	Thr	Asp	Ala	Gly	Ile	Leu	Gly	Thr	Thr	Lys	
				50					55					60	
Asp	Ser	Pro	Lys	Leu	Gly	Leu	Leu	Met	Val	Leu	Leu	Ser	Ile	Ile	
				65					70					75	
Phe	Met	Asn	Gly	Asn	Arg	Ser	Ser	Glu	Ala	Val	Ile	Trp	Glu	Val	
				80					85					90	
Leu	Arg	Lys	Leu	Gly	Leu	Arg	Pro	Gly	Ile	His	His	Ser	Leu	Phe	
				95					100					105	
Gly	Asp	Val	Lys	Lys	Leu	Ile	Thr	Asp	Glu	Phe	Val	Lys	Gln	Lys	
				110					115					120	
Tyr	Leu	Asp	Tyr	Ala	Arg	Val	Pro	Asn	Ser	Asn	Pro	Pro	Glu	Tyr	
				125					130					135	
Glu	Phe	Phe	Trp	Gly	Leu	Arg	Ser	Tyr	Tyr	Glu	Thr	Ser	Lys	Met	
				140					145					150	
Lys	Val	Leu	Lys	Phe	Ala	Cys	Lys	Val	Gln	Lys	Lys	Asp	Pro	Lys	

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Glu Trp Ala Ala	155	Gln Tyr Arg Glu Ala	160	Met Glu Ala Asp Leu	165
Ala Ala Ala Glu	170	Ala Ala Glu Ala	175	Lys Ala Arg Ala Glu	180
Arg Ala Arg Met	185	Gly Ile Gly Leu Gly	190	Ser Glu Asn Ala Ala	195
Pro Cys Asn Trp	200	Asp Glu Ala Asp Ile	205	Gly Pro Trp Ala Lys	210
Arg Ile Gln Ala	215	Gly Ala Glu Ala Lys	220	Ala Lys Ala Gln Glu	225
Gly Ser Ala Ser	230	Thr Gly Ala Ser Thr	235	Ser Thr Asn Asn Ser	240
Ser Ala Ser Ala	245	Ser Thr Ser Gly Gly	250	Phe Ser Ala Gly Ala	255
Leu Thr Ala Thr	260	Leu Thr Phe Gly Leu	265	Phe Ala Gly Leu Gly	270
Ala Gly Ala Ser	275	Thr Ser Gly Ser Ser	280	Gly Ala Cys Gly Phe	285
Tyr Lys	290		295		300

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTTUT01
- (B) CLONE: 1919931

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42 :

Met Arg Thr Leu Glu Asn Gln Gly Phe Lys Ile Leu Pro Phe Leu	5	10	15
Gly Val Lys Glu Val Trp Gln Lys Gln Asn Lys Leu Ile Ser Arg	20	25	30
Phe Ile Thr Cys Gln Phe Phe Leu Tyr Asn Phe Leu Asp Ser Gly	35	40	45
Ser Ile Trp Val Gln Ala Asp Phe Pro Pro Ile Leu Gln Cys Gly	50	55	60
Cys Phe Leu Phe His Pro Trp Thr Leu Gln Glu Ile Ala Pro Cys	65	70	75
Phe Cys Leu Cys Ile Thr Glu Lys Gly Ser Met Lys Val Ala Gln	80	85	90
Val Arg Pro Phe His Cys Pro Pro Gly Ala Gly Phe Ala Leu Pro	95	100	105
Ile Leu Gly Leu Leu Gln Gly Leu Val Ile Leu His Ser Pro Leu	110	115	120
His Ile Ser Gln Val Ser Ala Gln Lys Ser Pro Phe Gly Gly Val	125	130	135
Ser Thr Cys His Cys Val Cys Lys Ser Ser Phe Ser Phe Phe Leu	140	145	150
Ala His Leu Thr Leu Val Met Ser Leu Ile Thr Thr Thr Ile	155	160	

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTNOT04
- (B) CLONE: 1969426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43 :

Met	Ser	Pro	Thr	Leu	Ser	Ser	Ile	Thr	Gln	Gly	Val	Pro	Leu	Asp	5	10	15
Thr	Ser	Lys	Leu	Ser	Thr	Asp	Gln	Arg	Leu	Pro	Pro	Tyr	Pro	Tyr	20	25	30
Ser	Ser	Pro	Ser	Leu	Val	Leu	Pro	Thr	Gln	Pro	His	Thr	Pro	Lys	35	40	45
Ser	Leu	Gln	Gln	Pro	Gly	Leu	Pro	Ser	Gln	Ser	Cys	Ser	Val	Gln	50	55	60
Ser	Ser	Gly	Gly	Gln	Pro	Pro	Gly	Arg	Gln	Ser	His	Tyr	Gly	Thr	65	70	75
Pro	Tyr	Pro	Pro	Gly	Pro	Ser	Gly	His	Gly	Gln	Gln	Ser	Tyr	His	80	85	90
Arg	Pro	Met	Ser	Asp	Phe	Asn	Leu	Gly	Asn	Leu	Glu	Gln	Phe	Ser	95	100	105
Met	Glu	Ser	Pro	Ser	Ala	Ser	Leu	Val	Leu	Asp	Pro	Pro	Gly	Phe	110	115	120
Ser	Glu	Gly	Pro	Gly	Phe	Leu	Gly	Gly	Glu	Gly	Pro	Met	Gly	Gly	125	130	135
Pro	Gln	Asp	Pro	His	Thr	Phe	Asn	His	Gln	Asn	Leu	Thr	His	Cys	140	145	150
Ser	Arg	His	Gly	Ser	Gly	Pro	Asn	Ile	Ile	Leu	Thr	Gly	Asp	Ser	155	160	165
Ser	Pro	Gly	Phe	Ser	Lys	Glu	Ile	Ala	Ala	Ala	Leu	Ala	Gly	Val	170	175	180
Pro	Gly	Phe	Glu	Val	Ser	Ala	Ala	Gly	Leu	Glu	Leu	Gly	Leu	Gly	185	190	195
Leu	Glu	Asp	Glu	Leu	Arg	Met	Glu	Pro	Leu	Gly	Leu	Glu	Gly	Leu	200	205	210
Asn	Met	Leu	Ser	Asp	Pro	Cys	Ala	Leu	Leu	Pro	Asp	Pro	Ala	Val	215	220	225
Glu	Glu	Ser	Phe	Arg	Ser	Asp	Arg	Leu	Gln						230	235	

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: UCMCL5T01

(B) CLONE: 1969948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44 :

Met	Asn	Tyr	Phe	Pro	Leu	Ala	Pro	Phe	Asn	Gln	Leu	Leu	Gln	Lys	5	10	15
Asp	Ile	Ile	Ser	Glu	Leu	Leu	Thr	Ser	Asp	Asp	Met	Lys	Asn	Ala	20	25	30
Tyr	Lys	Leu	His	Thr	Leu	Asp	Thr	Cys	Leu	Lys	Leu	Asp	Asp	Thr	35	40	45
Val	Tyr	Leu	Arg	Asp	Ile	Ala	Leu	Ser	Leu	Pro	Gln	Leu	Pro	Arg	50	55	60
Glu	Leu	Pro	Ser	Ser	His	Thr	Asn	Ala	Lys	Val	Ala	Glu	Val	Leu	65	70	75
Ser	Ser	Leu	Leu	Gly	Gly	Glu	Gly	His	Phe	Ser	Lys	Asp	Val	His	80	85	90
Leu	Pro	His	Asn	Tyr	His	Ile	Asp	Phe	Glu	Ile	Arg	Met	Asp	Thr	95	100	105
Asn	Arg	Asn	Gln	Val	Leu	Pro	Leu	Ser	Asp	Val	Asp	Thr	Thr	Ser	110	115	120
Ala	Thr	Asp	Ile	Gln	Arg	Val	Ala	Val	Leu	Cys	Val	Ser	Arg	Ser	125	130	135
Ala	Tyr	Cys	Leu	Gly	Ser	Ser	His	Pro	Arg	Gly	Phe	Leu	Ala	Met	140	145	150
Lys	Met	Arg	His	Leu	Asn	Ala	Met	Gly	Phe	His	Val	Ile	Leu	Val	155	160	165
Asn	Asn	Trp	Glu	Met	Asp	Lys	Leu	Glu	Met	Glu	Asp	Ala	Val	Thr	170	175	180
Phe	Leu	Lys	Thr	Lys	Ile	Tyr	Ser	Val	Glu	Ala	Leu	Pro	Val	Ala	185	190	195
Ala	Val	Asn	Val	Gln	Ser	Thr	Gln								200		

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGAST01
- (B) CLONE: 1988911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45 :

Met	Glu	Arg	Gly	Asn	Val	Leu	Ser	Arg	Ala	Pro	Ser	Arg	Ala	His	5	10	15
Gly	Thr	His	Phe	Gly	Asp	Asp	Arg	Phe	Glu	Asp	Leu	Glu	Glu	Ala	20	25	30
Asn	Pro	Phe	Ser	Phe	Arg	Glu	Phe	Leu	Lys	Thr	Lys	Asn	Leu	Gly	35	40	45
Leu	Ser	Lys	Glu	Asp	Pro	Ala	Ser	Arg	Ile	Tyr	Ala	Lys	Glu	Ala	50	55	60
Ser	Arg	His	Ser	Leu	Gly	Leu	Asp	His	Asn	Ser	Pro	Pro	Ser	Gln	65	70	75
Thr	Gly	Gly	Tyr	Gly	Leu	Glu	Tyr	Gln	Gln	Pro	Phe	Phe	Glu	Asp			

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	80		85		90
Pro Thr Gly Ala Gly	Asp Leu Leu Asp	Glu Glu Glu Asp Glu	Asp		
	95		100		105
Thr Gly Trp Ser Gly	Ala Tyr Leu Pro	Ser Ala Ile Glu Gln Thr			
	110		115		120
His Pro Glu Arg Val	Pro Ala Gly Thr	Ser Pro Cys Ser Thr	Tyr		
	125		130		135
Leu Ser Phe Phe Ser	Thr Pro Ser Glu	Leu Ala Gly Pro Glu	Ser		
	140		145		150
Leu Pro Ser Trp Ala	Leu Ser Asp Thr	Asp Ser Arg Val Ser	Pro		
	155		160		165
Ala Ser Pro Ala Gly	Ser Pro Ser Ala	Asp Phe Ala Val His	Gly		
	170		175		180
Glu Ser Leu Gly Asp	Arg His Leu Arg	Thr Leu Gln Ile Ser	Tyr		
	185		190		195
Asp Ala Leu Lys Asp	Glu Asn Ser Lys	Leu Arg Arg Lys Leu	Asn		
	200		205		210
Glu Val Gln Ser Phe	Ser Glu Ala Gln	Thr Glu Met Val Arg	Thr		
	215		220		225
Leu Glu Arg Lys Leu	Glu Ala Lys Met	Ile Lys Glu Glu Ser	Asp		
	230		235		240
Tyr His Asp Leu Glu	Ser Val Val Gln	Gln Val Glu Gln Asn	Leu		
	245		250		255
Glu Leu Met Thr Lys	Arg Ala Val Lys	Ala Glu Asn His Val	Val		
	260		265		270
Lys Leu Lys Gln Glu	Ile Ser Leu Leu	Gln Ala Gln Val Ser	Asn		
	275		280		285
Phe Gln Arg Glu Asn	Glu Ala Leu Arg	Cys Gly Gln Gly Ala	Ser		
	290		295		300
Leu Thr Val Val Lys	Gln Asn Ala Asp	Val Ala Leu Gln Asn	Leu		
	305		310		315
Arg Val Val Met Asn	Ser Ala Gln Ala	Ser Ile Lys Gln Leu	Val		
	320		325		330
Ser Gly Ala Glu Thr	Leu Asn Leu Val	Ala Glu Ile Leu Lys	Ser		
	335		340		345
Ile Asp Arg Ile Ser	Glu Val Lys Asp	Glu Glu Glu Asp Ser			
	350		355		

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: OVARNOT03
- (B) CLONE: 2061561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46 :

Met Gly Gly Lys Pro	His Lys Glu Pro	Arg Ala Lys Gly Pro	Leu
	5	10	15
Ser Ile Phe Tyr Pro	Gly Ser Thr Ala	Pro Val Ile Thr Gln	Arg
	20	25	30
Thr Pro Xaa Ala Ala	Leu Lys Pro Pro	Pro Ile Lys Gly Ala	Gly
	35	40	45

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Pro	Thr	Ile	Ala	Pro	Ile	Lys	Gly	Xaa	Xaa	Asn	Phe	Gly	Lys	Arg
				50					55					60
Pro	Thr	Val	Thr	Xaa	Pro	Xaa	Trp	Xaa	Ile	Ser	Pro	Asn	Trp	Gly
				65					70					75
Lys	Arg	Gly	Xaa	Cys	Xaa	Xaa	Xaa	Gly	Ile	Lys	Trp	Val	Xaa	Pro
				80					85					90
Arg	Val	Ser	Gln	Ala	Arg	Thr	Phe	Lys	Thr	Thr	Ala	Asn	Glu	Leu
				95					100					105
Xaa	Phe	Xaa	Asp	Thr	Phe	Glu	Glu	Xaa	Xaa	Arg	Xaa	Xaa	His	Ala
				110					115					120
Xaa	Val	Ser	Xaa	Glu	Pro	Gln	Pro	Arg	Cys	Pro	Leu	Gly	Glu	Ser
				125					130					135
Arg	Ser	Leu	Gly	Ala	Ala	Val	Cys	Arg	Trp	Asp	Ser	Phe	Asp	Phe
				140					145					150

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PANCNOT04
- (B) CLONE: 2084489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47 :

Met	Pro	Pro	Val	Ser	Arg	Ser	Ser	Tyr	Ser	Glu	Asp	Ile	Val	Gly
				5					10					15
Ser	Arg	Arg	Arg	Arg	Arg	Ser	Ser	Ser	Gly	Ser	Pro	Pro	Ser	Pro
				20					25					30
Gln	Ser	Arg	Cys	Ser	Ser	Trp	Asp	Gly	Cys	Ser	Arg	Ser	His	Ser
				35					40					45
Arg	Gly	Arg	Glu	Gly	Leu	Arg	Pro	Pro	Trp	Ser	Glu	Leu	Asp	Val
				50					55					60
Gly	Ala	Leu	Tyr	Pro	Phe	Ser	Arg	Ser	Gly	Ser	Arg	Gly	Arg	Leu
				65					70					75
Pro	Arg	Phe	Arg	Asn	Tyr	Ala	Phe	Ala	Ser	Ser	Trp	Ser	Thr	Ser
				80					85					90
Tyr	Ser	Gly	Tyr	Arg	Tyr	His	Arg	His	Cys	Tyr	Ala	Glu	Glu	Arg
				95					100					105
Gln	Ser	Ala	Glu	Asp	Tyr	Glu	Lys	Glu	Glu	Ser	His	Arg	Gln	Arg
				110					115					120
Arg	Leu	Lys	Glu	Arg	Glu	Arg	Ile	Gly	Glu	Leu	Gly	Ala	Pro	Glu
				125					130					135
Val	Trp	Gly	Pro	Ser	Pro	Lys	Phe	Pro	Gln	Leu	Asp	Ser	Asp	Glu
				140					145					150
His	Thr	Pro	Val	Glu	Asp	Glu	Glu	Glu	Val	Thr	His	Gln	Lys	Ser
				155					160					165
Ser	Ser	Ser	Asp	Ser	Asn	Ser	Glu	Glu	His	Arg	Lys	Lys	Lys	Thr
				170					175					180
Ser	Arg	Ser	Arg	Asn	Lys	Lys	Lys	Arg	Lys	Asn	Lys	Ser	Ser	Lys
				185					190					195
Arg	Lys	His	Arg	Lys	Tyr	Ser	Asp	Ser	Asp	Ser	Asn	Ser	Glu	Ser

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Asp Thr Asn Ser	200	Asp Ser Asp Asp Asp	205	Lys Lys Arg Val Lys	210
Lys Lys Lys Lys	215	Lys Lys Lys His	220	Thr Lys Lys Lys	225
Asn Lys Lys Thr	230	Lys Lys Glu Ser Ser	235	Asp Ser Ser Cys Lys	240
Ser Glu Glu Asp	245	Leu Ser Glu Ala Thr	250	Trp Met Glu Gln Pro	255
Val Ala Asp Thr	260	Met Asp Leu Ile Gly	265	Pro Glu Ala Pro Ile	270
His Thr Ser Gln	275	Asp Glu Lys Pro Leu	280	Lys Tyr Gly His Ala	285
Leu Pro Gly Glu	290	Gly Ala Ala Met Ala	295	Glu Tyr Val Lys Ala	300
Lys Arg Ile Pro	305	Arg Arg Gly Glu Ile	310	Gly Leu Thr Ser Glu	315
Ile Gly Ser Phe	320	Glu Cys Ser Gly Tyr	325	Val Met Ser Gly Ser	330
His Arg Arg Met	335	Glu Ala Val Arg Leu	340	Arg Lys Glu Asn Gln	345
Tyr Ser Ala Asp	350	Glu Lys Arg Ala Leu	355	Ala Ser Phe Asn Gln	360
Glu Arg Arg Lys	365	Arg Glu Ser Lys Ile	370	Leu Ala Ser Phe Arg	375
Met Val His Lys	380	Lys Thr Lys Glu Lys	385	Asp Asp Lys	390
	395		400		

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SPLNFET02
- (B) CLONE: 2203226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48 :

Met His Pro Ala Gly	Leu Ala Ala Ala	Ala Ala Gly Thr	Pro Arg
	5	10	15
Leu Pro Ser Lys Arg	Arg Ile Pro Val	Ser Gln Pro Gly	Met Ala
	20	25	30
Asp Pro His Gln Leu	Phe Asp Asp Thr	Ser Ser Ala Gln	Ser Arg
	35	40	45
Gly Tyr Gly Ala Gln	Arg Ala Pro Gly	Gly Leu Ser Tyr	Pro Ala
	50	55	60
Ala Ser Pro Thr Pro	His Ala Ala Phe	Leu Ala Asp Pro	Val Ser
	65	70	75
Asn Met Ala Met Ala	Tyr Gly Ser Ser	Leu Ala Ala Gln	Gly Lys
	80	85	90
Glu Leu Val Asp Lys	Asn Ile Asp Arg	Phe Ile Pro Ile	Thr Lys
	95	100	105
Leu Lys Tyr Tyr Phe	Ala Val Asp Thr	Met Tyr Val Gly	Arg Lys
	110	115	120

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Leu	Gly	Leu	Leu	Phe	Phe	Pro	Tyr	Leu	His	Gln	Asp	Trp	Glu	Val	
				125					130					135	
Gln	Tyr	Gln	Gln	Asp	Thr	Pro	Val	Ala	Pro	Arg	Phe	Asp	Val	Asn	
				140					145					150	
Ala	Pro	Asp	Leu	Tyr	Ile	Pro	Ala	Met	Ala	Phe	Ile	Thr	Tyr	Val	
				155					160					165	
Leu	Val	Ala	Gly	Leu	Ala	Leu	Gly	Thr	Gln	Asp	Arg	Phe	Ser	Pro	
				170					175					180	
Asp	Leu	Leu	Gly	Leu	Gln	Ala	Ser	Ser	Ala	Leu	Ala	Trp	Leu	Thr	
				185					190					195	
Leu	Glu	Val	Leu	Ala	Ile	Leu	Leu	Ser	Leu	Tyr	Leu	Val	Thr	Val	
				200					205					210	
Asn	Thr	Asp	Leu	Thr	Thr	Ile	Asp	Leu	Val	Ala	Phe	Leu	Gly	Tyr	
				215					220					225	
Lys	Tyr	Val	Gly	Met	Ile	Gly	Gly	Val	Leu	Met	Gly	Leu	Leu	Phe	
				230					235					240	
Gly	Lys	Ile	Gly	Tyr	Tyr	Leu	Val	Leu	Gly	Trp	Cys	Cys	Val	Ala	
				245					250					255	
Ile	Phe	Val	Phe	Met	Ile	Arg	Thr	Leu	Arg	Leu	Lys	Ile	Leu	Ala	
				260					265					270	
Asp	Ala	Ala	Ala	Glu	Gly	Val	Pro	Val	Arg	Gly	Ala	Arg	Asn	Gln	
				275					280					285	
Leu	Arg	Met	Tyr	Leu	Thr	Met	Ala	Val	Ala	Ala	Ala	Gln	Pro	Met	
				290					295					300	
Leu	Met	Tyr	Trp	Leu	Thr	Phe	His	Leu	Val	Arg					
				305					310						

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNOT16
- (B) CLONE: 2232884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49 :

Met	Ala	Ser	Ala	Asp	Glu	Leu	Thr	Phe	His	Glu	Phe	Glu	Glu	Ala	
				5					10					15	
Thr	Asn	Leu	Leu	Ala	Asp	Thr	Pro	Asp	Ala	Ala	Thr	Thr	Ser	Arg	
				20					25					30	
Ser	Asp	Gln	Leu	Thr	Pro	Gln	Gly	His	Val	Ala	Val	Ala	Val	Gly	
				35					40					45	
Ser	Gly	Gly	Ser	Tyr	Gly	Ala	Glu	Asp	Glu	Val	Glu	Glu	Glu	Ser	
				50					55					60	
Asp	Lys	Ala	Ala	Leu	Leu	Gln	Glu	Gln	Gln	Gln	Gln	Gln	Gln	Pro	
				65					70					75	
Gly	Phe	Trp	Thr	Phe	Ser	Tyr	Tyr	Gln	Ser	Phe	Phe	Asp	Val	Asp	
				80					85					90	
Thr	Ser	Gln	Val	Leu	Asp	Arg	Ile	Lys	Gly	Ser	Leu	Leu	Pro	Arg	
				95					100					105	
Pro	Gly	His	Asn	Phe	Val	Arg	His	His	Leu	Arg	Asn	Arg	Pro	Asp	
				110					115					120	
Leu	Tyr	Gly	Pro	Phe	Trp	Ile	Cys	Ala	Thr	Leu	Ala	Phe	Val	Leu	

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Ala	Val	Thr	Gly	125	Asn	Leu	Thr	Leu	Val	130	Leu	Ala	Gln	Arg	Arg	Asp	135
Pro	Ser	Ile	His	140	Tyr	Ser	Pro	Gln	Phe	145	His	Lys	Val	Thr	Val	Ala	150
Gly	Ile	Ser	Ile	155	Tyr	Cys	Tyr	Ala	Trp	160	Leu	Val	Pro	Leu	Ala	Leu	165
Trp	Gly	Phe	Leu	170	Arg	Trp	Arg	Lys	Gly	175	Val	Gln	Glu	Arg	Met	Gly	180
Pro	Tyr	Thr	Phe	185	Leu	Glu	Thr	Val	Cys	190	Ile	Tyr	Gly	Tyr	Ser	Leu	195
Phe	Val	Phe	Ile	200	Pro	Met	Val	Val	Leu	205	Trp	Leu	Ile	Pro	Val	Pro	210
Trp	Leu	Gln	Trp	215	Leu	Phe	Gly	Ala	Leu	220	Ala	Leu	Gly	Leu	Ser	Ala	225
Ala	Gly	Leu	Val	230	Phe	Thr	Leu	Trp	Pro	235	Val	Val	Arg	Glu	Asp	Thr	240
Arg	Leu	Val	Ala	245	Thr	Val	Leu	Leu	Ser	250	Val	Val	Val	Leu	Leu	His	255
Ala	Leu	Leu	Ala	260	Met	Gly	Cys	Lys	Leu	265	Tyr	Phe	Phe	Gln	Ser	Leu	270
Pro	Pro	Glu	Asn	275	Val	Ala	Pro	Pro	Pro	280	Gln	Ile	Thr	Ser	Leu	Pro	285
Ser	Asn	Ile	Ala	290	Leu	Ser	Pro	Thr	Leu	295	Pro	Gln	Ser	Leu	Ala	Pro	300
Ser				305						310							315

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNNOT11
- (B) CLONE: 2328134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50 :

Met	Thr	Pro	Arg	Thr	Trp	Trp	Pro	Arg	Pro	Ala	Gly	Trp	Gly	Thr			
				5					10					15			
Cys	Arg	Ala	Ala	Gly	Trp	Pro	Arg	Ser	Val	Pro	Trp	Ala	Arg	Thr			
				20					25					30			
Ala	Ala	Ser	Leu	Val	Phe	Val	Pro	Thr	Arg	Arg	Arg	Ser	Gly	Pro			
				35					40					45			
Ser	Gly	Thr	Ala	Ser	Val	Ala	Ala	Met	Ala	Tyr	His	Ser	Gly	Tyr			
				50					55					60			
Gly	Ala	His	Gly	Ser	Lys	His	Arg	Ala	Arg	Ala	Ala	Pro	Asp	Pro			
				65					70					75			
Pro	Pro	Leu	Phe	Asp	Asp	Thr	Ser	Gly	Gly	Tyr	Ser	Ser	Gln	Pro			
				80					85					90			
Gly	Gly	Tyr	Pro	Ala	Thr	Gly	Ala	Asp	Val	Ala	Phe	Ser	Val	Asn			
				95					100					105			
His	Leu	Leu	Gly	Asp	Pro	Met	Ala	Asn	Val	Ala	Met	Ala	Tyr	Gly			
				110					115					120			
Ser	Ser	Ile	Ala	Ser	His	Gly	Lys	Asp	Met	Val	His	Lys	Glu	Leu			
				125					130					135			

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His	Arg	Phe	Val	Ser	Val	Ser	Lys	Leu	Lys	Tyr	Phe	Phe	Ala	Val
				140					145					150
Asp	Thr	Ala	Tyr	Val	Ala	Lys	Lys	Leu	Gly	Leu	Leu	Val	Phe	Pro
				155					160					165
Tyr	Thr	His	Gln	Asn	Trp	Glu	Val	Gln	Tyr	Ser	Arg	Asp	Ala	Pro
				170					175					180
Leu	Pro	Pro	Arg	Gln	Asp	Leu	Asn	Ala	Pro	Asp	Leu	Tyr	Ile	Pro
				185					190					195
Thr	Met	Ala	Phe	Ile	Thr	Tyr	Val	Leu	Leu	Ala	Gly	Met	Ala	Leu
				200					205					210
Gly	Ile	Gln	Lys	Arg	Phe	Ser	Pro	Glu	Val	Leu	Gly	Leu	Cys	Ala
				215					220					225
Ser	Thr	Ala	Leu	Val	Trp	Val	Val	Met	Glu	Val	Leu	Ala	Leu	Leu
				230					235					240
Leu	Gly	Leu	Tyr	Leu	Ala	Thr	Val	Arg	Ser	Asp	Leu	Ser	Thr	Phe
				245					250					255
His	Leu	Leu	Ala	Tyr	Ser	Gly	Tyr	Lys	Tyr	Val	Gly	Met	Ile	Leu
				260					265					270
Ser	Val	Leu	Thr	Gly	Leu	Leu	Phe	Gly	Ser	Asp	Gly	Tyr	Tyr	Val
				275					280					285
Ala	Leu	Ala	Trp	Thr	Ser	Ser	Ala	Leu	Met	Tyr	Phe	Ile	Val	Arg
				290					295					300
Ser	Leu	Arg	Thr	Ala	Ala	Leu	Gly	Pro	Asp	Ser	Met	Gly	Gly	Pro
				305					310					315
Val	Pro	Arg	Gln	Arg	Leu	Gln	Leu	Tyr	Leu	Thr	Leu	Gly	Ala	Ala
				320					325					330
Ala	Phe	Gln	Pro	Leu	Ile	Ile	Tyr	Trp	Leu	Thr	Phe	His	Leu	Val
				335					340					345

Arg

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: ISLTNOT01
- (B) CLONE: 2382718

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51 :

Met	Gly	Thr	Lys	Ala	Gln	Val	Glu	Arg	Lys	Leu	Leu	Cys	Leu	Phe
				5					10					15
Ile	Leu	Ala	Ile	Leu	Leu	Cys	Ser	Leu	Ala	Leu	Gly	Ser	Val	Thr
				20					25					30
Val	His	Ser	Ser	Glu	Pro	Glu	Val	Arg	Ile	Pro	Glu	Asn	Asn	Pro
				35					40					45
Val	Lys	Leu	Ser	Cys	Ala	Tyr	Ser	Gly	Phe	Ser	Ser	Pro	Arg	Val
				50					55					60
Glu	Trp	Lys	Phe	Asp	Gln	Gly	Asp	Thr	Thr	Arg	Leu	Val	Cys	Tyr
				65					70					75
Asn	Asn	Lys	Ile	Thr	Ala	Ser	Tyr	Glu	Asp	Arg	Val	Thr	Phe	Leu
				80					85					90
Pro	Thr	Gly	Ile	Thr	Phe	Lys	Ser	Val	Thr	Arg	Glu	Asp	Thr	Gly
				95					100					105
Thr	Tyr	Thr	Cys	Met	Val	Ser	Glu	Glu	Gly	Gly	Asn	Ser	Tyr	Gly

	110		115		120
Glu Val Lys Val	Lys Leu Ile Val Leu	Val Pro Pro Ser Lys	Pro		
	125		130		135
Thr Val Asn Ile	Pro Ser Ser Ala Thr	Ile Gly Asn Arg Ala	Val		
	140		145		150
Leu Thr Cys Ser	Glu Gln Asp Gly Ser	Pro Pro Ser Glu Tyr	Thr		
	155		160		165
Trp Phe Lys Asp	Gly Ile Val Met Pro	Thr Asn Pro Lys Ser	Thr		
	170		175		180
Arg Ala Phe Ser	Asn Ser Ser Tyr Val	Leu Asn Pro Thr Thr	Gly		
	185		190		195
Glu Leu Val Phe	Asp Pro Leu Ser Ala	Ser Asp Thr Gly Glu	Tyr		
	200		205		210
Ser Cys Glu Ala	Arg Asn Gly Tyr Gly	Thr Pro Met Thr Ser	Asn		
	215		220		225
Ala Val Arg Met	Glu Ala Val Glu Arg	Asn Val Gly Val Ile	Val		
	230		235		240
Ala Ala Val Leu	Val Thr Leu Ile Leu	Leu Gly Ile Leu Val	Phe		
	245		250		255
Gly Ile Trp Phe	Ala Tyr Ser Arg Gly	His Phe Asp Arg Thr	Lys		
	260		265		270
Lys Gly Thr Ser	Ser Lys Lys Val Ile	Tyr Ser Gln Pro Ser	Ala		
	275		280		285
Arg Ser Glu Gly	Glu Phe Lys Gln Thr	Ser Ser Phe Leu Val			
	290		295		

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: ENDANOT01
- (B) CLONE: 2452208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52 :

Met Ala Ser Thr Gly	Ser Gln Ala Ser Asp	Ile Asp Glu Ile Phe	
	5	10	15
Gly Phe Phe Asn Asp	Gly Glu Pro Pro Thr	Lys Lys Pro Arg Lys	
	20	25	30
Leu Leu Pro Ser Leu	Lys Thr Lys Lys Pro	Arg Glu Leu Val Leu	
	35	40	45
Val Ile Gly Thr Gly	Ile Ser Ala Ala Val	Ala Pro Gln Val Pro	
	50	55	60
Ala Leu Lys Ser Trp	Lys Gly Leu Ile Gln	Ala Leu Leu Asp Ala	
	65	70	75
Ala Ile Asp Phe Asp	Leu Leu Glu Asp Glu	Glu Ser Lys Lys Phe	
	80	85	90
Gln Lys Cys Leu His	Glu Asp Lys Asn Leu	Val His Val Ala His	
	95	100	105
Asp Leu Ile Gln Lys	Leu Ser Pro Arg Thr	Ser Asn Val Arg Ser	
	110	115	120
Thr Phe Phe Lys Asp	Cys Leu Tyr Glu Val	Phe Asp Asp Leu Glu	
	125	130	135

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Ser	Lys	Met	Glu	Asp	Ser	Gly	Lys	Gln	Leu	Leu	Gln	Ser	Val	Leu
				140					145					150
His	Leu	Met	Glu	Asn	Gly	Ala	Leu	Val	Leu	Thr	Thr	Asn	Phe	Asp
				155					160					165
Asn	Leu	Leu	Glu	Leu	Tyr	Ala	Ala	Asp	Gln	Gly	Lys	Gln	Leu	Glu
				170					175					180
Ser	Leu	Asp	Leu	Thr	Asp	Glu	Lys	Lys	Val	Leu	Glu	Trp	Ala	Gln
				185					190					195
Glu	Lys	Arg	Lys	Leu	Ser	Val	Leu	His	Ile	His	Gly	Val	Tyr	Thr
				200					205					210
Asn	Pro	Ser	Gly	Ile	Val	Leu	His	Pro	Ala	Gly	Tyr	Gln	Asn	Val
				215					220					225
Leu	Arg	Asn	Thr	Glu	Val	Met	Arg	Glu	Ile	Gln	Lys	Leu	Tyr	Glu
				230					235					240
Asn	Lys	Ser	Phe	Leu	Phe	Leu	Gly	Cys	Gly	Trp	Thr	Val	Asp	Asp
				245					250					255
Thr	Thr	Phe	Gln	Ala	Leu	Phe	Leu	Glu	Ala	Val	Lys	His	Lys	Ser
				260					265					270
Asp	Leu	Glu	His	Phe	Met	Leu	Val	Arg	Arg	Gly	Asp	Val	Asp	Glu
				275					280					285
Phe	Lys	Lys	Leu	Arg	Glu	Asn	Met	Leu	Asp	Lys	Gly	Ile	Lys	Val
				290					295					300
Ile	Ser	Tyr	Gly	Asp	Asp	Tyr	Ala	Asp	Leu	Pro	Glu	Tyr	Phe	Lys
				305					310					315
Arg	Leu	Thr	Cys	Glu	Ile	Ser	Thr	Arg	Gly	Thr	Ser	Ala	Gly	Met
				320					325					330
Val	Arg	Glu	Gly	Gln	Leu	Asn	Gly	Ser	Ser	Ala	Ala	His	Ser	Glu
				335					340					345
Ile	Arg	Gly	Cys	Ser	Thr									
				350										

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 662 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: ENDANOT01
- (B) CLONE: 2457825

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53 :

Met	Thr	Ala	Lys	Lys	Gln	Cys	Leu	Leu	Arg	Leu	Gly	Val	Leu	Arg
				5					10					15
Gln	Asp	Trp	Pro	Asp	Thr	Asn	Arg	Leu	Leu	Gly	Ser	Ala	Asn	Val
				20					25					30
Val	Pro	Glu	Ala	Leu	Gln	Arg	Phe	Thr	Arg	Ala	Ala	Ala	Asp	Phe
				35					40					45
Ala	Thr	His	Gly	Lys	Leu	Gly	Lys	Leu	Glu	Phe	Ala	Gln	Asp	Ala
				50					55					60
His	Gly	Gln	Pro	Asp	Val	Ser	Ala	Phe	Asp	Phe	Thr	Ser	Met	Met
				65					70					75
Arg	Ala	Glu	Ser	Ser	Ala	Arg	Val	Gln	Glu	Lys	His	Gly	Ala	Arg
				80					85					90
Leu	Leu	Leu	Gly	Leu	Val	Gly	Asp	Cys	Leu	Val	Glu	Pro	Phe	Trp

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Pro	Leu	Gly	Thr	95	Gly	Val	Ala	Arg	Gly	100	Phe	Leu	Ala	Ala	Phe	Asp	105
				110						115							120
Ala	Ala	Trp	Met	125	Val	Lys	Arg	Trp	Ala	130	Glu	Gly	Ala	Glu	Ser	Leu	135
Glu	Val	Leu	Ala	140	Glu	Arg	Glu	Ser	Leu	145	Tyr	Gln	Leu	Leu	Ser	Gln	150
Thr	Ser	Pro	Glu	155	Asn	Met	His	Arg	Asn	160	Val	Ala	Gln	Tyr	Gly	Leu	165
Asp	Pro	Ala	Thr	170	Arg	Tyr	Pro	Asn	Leu	175	Asn	Leu	Arg	Ala	Val	Thr	180
Pro	Asn	Gln	Val	185	Arg	Asp	Leu	Tyr	Asp	190	Val	Leu	Ala	Lys	Glu	Pro	195
Val	Gln	Arg	Asp	200	Asn	Asp	Lys	Thr	Asp	205	Thr	Gly	Met	Pro	Ala	Thr	210
Gly	Ser	Ala	Gly	215	Thr	Gln	Glu	Glu	Leu	220	Leu	Arg	Trp	Cys	Gln	Glu	225
Gln	Thr	Ala	Gly	230	Tyr	Pro	Gly	Val	His	235	Val	Ser	Asp	Leu	Ser	Ser	240
Ser	Trp	Ala	Asp	245	Gly	Leu	Ala	Leu	Cys	250	Ala	Leu	Val	Tyr	Arg	Leu	255
Gln	Pro	Gly	Leu	260	Leu	Glu	Pro	Ser	Glu	265	Leu	Gln	Gly	Leu	Gly	Ala	270
Leu	Glu	Ala	Thr	275	Ala	Trp	Ala	Leu	Lys	280	Val	Ala	Glu	Asn	Glu	Leu	285
Gly	Ile	Thr	Pro	290	Val	Val	Ser	Ala	Gln	295	Ala	Val	Val	Ala	Gly	Ser	300
Asp	Pro	Leu	Gly	305	Leu	Ile	Ala	Tyr	Leu	310	Ser	His	Phe	His	Ser	Ala	315
Phe	Lys	Ser	Met	320	Ala	His	Ser	Pro	Gly	325	Pro	Val	Ser	Gln	Ala	Ser	330
Pro	Gly	Thr	Ser	335	Ser	Ala	Val	Leu	Phe	340	Leu	Ser	Lys	Leu	Gln	Arg	345
Thr	Leu	Gln	Arg	350	Ser	Arg	Ala	Lys	Glu	355	Asn	Ala	Glu	Asp	Ala	Gly	360
Gly	Lys	Lys	Leu	365	Arg	Leu	Glu	Met	Glu	370	Ala	Glu	Thr	Pro	Ser	Thr	375
Glu	Val	Pro	Pro	380	Asp	Pro	Glu	Pro	Gly	385	Val	Pro	Leu	Thr	Pro	Pro	390
Ser	Gln	His	Gln	395	Glu	Ala	Gly	Ala	Gly	400	Asp	Leu	Cys	Ala	Leu	Cys	405
Gly	Glu	His	Leu	410	Tyr	Val	Leu	Glu	Arg	415	Leu	Cys	Val	Asn	Gly	His	420
Phe	Phe	His	Arg	425	Ser	Cys	Phe	Arg	Cys	430	His	Thr	Cys	Glu	Ala	Thr	435
Leu	Trp	Pro	Gly	440	Gly	Tyr	Glu	Gln	His	445	Pro	Gly	Ser	Arg	Thr	Ser	450
Gln	Phe	Phe	Phe	455	Ser	Ala	Leu	Val	Ala	460	Met	Glu	Lys	Glu	Glu	Lys	465
Glu	Ser	Pro	Phe	470	Ser	Ser	Glu	Glu	Glu	475	Glu	Glu	Asp	Val	Pro	Leu	480
Asp	Ser	Asp	Val	485	Glu	Gln	Ala	Leu	Gln	490	Thr	Phe	Ala	Lys	Thr	Ser	495
Gly	Thr	Met	Asn	500	Asn	Tyr	Pro	Thr	Trp	505	Arg	Arg	Thr	Leu	Leu	Arg	510
Arg	Ala	Lys	Glu	515	Glu	Glu	Met	Lys	Arg	520	Phe	Cys	Lys	Ala	Gln	Thr	525
Ile	Gln	Arg	Arg	530	Leu	Asn	Glu	Ile	Glu	535	Ala	Ala	Leu	Arg	Glu	Leu	540
Glu	Ala	Glu	Gly	545	Val	Lys	Leu	Glu	Leu	550	Ala	Leu	Arg	Arg	Gln	Ser	555

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Ser	Ser	Pro	Glu	Gln	Gln	Lys	Lys	Leu	Trp	Val	Gly	Gln	Leu	Leu
				560					565					570
Gln	Leu	Val	Asp	Lys	Lys	Asn	Ser	Leu	Val	Ala	Glu	Glu	Ala	Glu
				575					580					585
Leu	Met	Ile	Thr	Val	Gln	Glu	Leu	Asn	Leu	Glu	Glu	Lys	Gln	Trp
				590					595					600
Gln	Leu	Asp	Gln	Glu	Leu	Arg	Gly	Tyr	Met	Asn	Arg	Glu	Glu	Asn
				605					610					615
Leu	Lys	Thr	Ala	Ala	Asp	Arg	Gln	Ala	Glu	Asp	Gln	Val	Leu	Arg
				620					625					630
Lys	Leu	Val	Asp	Leu	Val	Asn	Gln	Arg	Asp	Ala	Leu	Ile	Arg	Phe
				635					640					645
Gln	Glu	Glu	Arg	Arg	Leu	Ser	Glu	Leu	Ala	Leu	Gly	Thr	Gly	Ala
				650					655					660
Gln	Gly													

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THP1NOT03
- (B) CLONE: 2470740

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54 :

Met	Ala	Ser	Trp	Pro	Ala	Ser	Pro	Leu	Gln	Trp	Gly	Pro	Pro	Leu
				5					10					15
Ala	Ser	Cys	Pro	Ser	Cys	Cys	Cys	Cys	Cys	Phe	His	Cys	Trp	Gln
				20					25					30
Pro	Arg	Val	Gly	Val	Ala	Cys	Arg	Gln	Arg	Cys	Trp	Pro	Leu	Arg
				35					40					45
Trp	Gly	Trp	Trp	Val	Trp	Gly	Pro	Pro	Thr	Cys	Ser	Phe	Val	Gln
				50					55					60
Pro	Cys	Thr	Cys	Pro	Pro	Val	Phe	Ser	Tyr	Ser	Trp	Pro	Arg	Val
				65					70					75
Pro	His	Trp	Gly	Pro	Ser	Trp	Xaa	Met	Ser	Trp	Arg	Arg	Arg	Leu
				80					85					90
Met	Gly	Val	Pro	Leu	Gly	Leu	Trp	Asn	Cys	Leu	Val	Leu	Lys	Leu
				95					100					105
Xaa	Gln	Gly	Leu	Ala	Pro	Thr	Ser	Gly	Gly					
				110					115					

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

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(A) LIBRARY: SMCANOT01

(B) CLONE: 2479092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55 :

Met	Glu	Ala	Leu	Arg	Arg	Ala	His	Glu	Val	Ala	Leu	Arg	Leu	Leu	
			5						10						15
Leu	Cys	Arg	Pro	Trp	Ala	Ser	Arg	Ala	Ala	Ala	Arg	Pro	Lys	Pro	
			20						25						30
Ser	Ala	Ser	Glu	Val	Leu	Thr	Arg	His	Leu	Leu	Gln	Arg	Arg	Leu	
			35						40						45
Pro	His	Trp	Thr	Ser	Phe	Cys	Val	Pro	Tyr	Ser	Ala	Val	Arg	Asn	
			50						55						60
Asp	Gln	Phe	Gly	Leu	Ser	His	Phe	Asn	Trp	Pro	Val	Gln	Gly	Ala	
			65						70						75
Asn	Tyr	His	Val	Leu	Arg	Thr	Gly	Cys	Phe	Pro	Phe	Ile	Lys	Tyr	
			80						85						90
His	Cys	Ser	Lys	Ala	Pro	Trp	Gln	Asp	Leu	Ala	Arg	Gln	Asn	Arg	
			95						100						105
Phe	Phe	Thr	Ala	Leu	Lys	Val	Val	Asn	Leu	Gly	Ile	Pro	Thr	Leu	
			110						115						120
Leu	Tyr	Gly	Leu	Gly	Ser	Trp	Leu	Phe	Ala	Arg	Val	Thr	Glu	Thr	
			125						130						135
Val	His	Thr	Ser	Tyr	Gly	Pro	Ile	Thr	Val	Tyr	Phe	Leu	Asn	Lys	
			140						145						150
Glu	Asp	Glu	Gly	Ala	Met	Tyr									
			155												

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: SMCANOT01

(B) CLONE: 2480544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56 :

Met	Pro	Pro	Ala	Gly	Leu	Arg	Arg	Ala	Ala	Pro	Leu	Thr	Ala	Ile	
			5						10						15
Ala	Leu	Leu	Val	Leu	Gly	Ala	Pro	Leu	Val	Leu	Ala	Gly	Glu	Asp	
			20						25						30
Cys	Leu	Trp	Tyr	Leu	Asp	Arg	Asn	Gly	Ser	Trp	His	Pro	Gly	Phe	
			35						40						45
Asn	Cys	Glu	Phe	Phe	Thr	Phe	Cys	Cys	Gly	Thr	Cys	Tyr	His	Arg	
			50						55						60
Tyr	Cys	Cys	Arg	Asp	Leu	Thr	Leu	Leu	Ile	Thr	Glu	Arg	Gln	Gln	
			65						70						75
Lys	His	Cys	Leu	Ala	Phe	Ser	Pro	Lys	Thr	Ile	Ala	Gly	Ile	Ala	
			80						85						90
Ser	Ala	Val	Ile	Leu	Phe	Val	Ala	Val	Val	Ala	Thr	Thr	Ile	Cys	
			95						100						105
Cys	Phe	Leu	Cys	Ser	Cys	Cys	Tyr	Leu	Tyr	Arg	Arg	Arg	Gln	Gln	
			110						115						120

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Leu	Gln	Ser	Pro	Phe	Glu	Gly	Gln	Glu	Ile	Pro	Met	Thr	Gly	Ile
				125					130					135
Pro	Val	Gln	Pro	Val	Tyr	Pro	Tyr	Pro	Gln	Asp	Pro	Lys	Ala	Gly
				140					145					150
Pro	Ala	Pro	Pro	Gln	Pro	Gly	Phe	Met	Tyr	Pro	Pro	Ser	Gly	Pro
				155					160					165
Ala	Pro	Gln	Tyr	Pro	Leu	Tyr	Pro	Ala	Gly	Pro	Pro	Val	Tyr	Asn
				170					175					180
Pro	Ala	Ala	Pro	Pro	Pro	Tyr	Met	Pro	Pro	Gln	Pro	Ser	Tyr	Pro
				185					190					195
Gly	Ala													

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAITUT21
- (B) CLONE: 2518547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57 :

Met	Gly	Gly	Ala	Ser	Arg	Arg	Val	Glu	Ser	Gly	Ala	Trp	Ala	Tyr
				5					10					15
Leu	Ser	Pro	Leu	Val	Leu	Arg	Lys	Glu	Leu	Glu	Ser	Leu	Val	Glu
				20					25					30
Asn	Glu	Gly	Ser	Glu	Val	Leu	Ala	Leu	Pro	Glu	Leu	Pro	Ser	Ala
				35					40					45
His	Pro	Ile	Ile	Phe	Trp	Asn	Leu	Leu	Trp	Tyr	Phe	Gln	Arg	Leu
				50					55					60
Arg	Leu	Pro	Ser	Ile	Leu	Pro	Gly	Leu	Val	Leu	Ala	Ser	Cys	Asp
				65					70					75
Gly	Pro	Ser	His	Ser	Gln	Ala	Pro	Ser	Pro	Trp	Leu	Thr	Pro	Asp
				80					85					90
Pro	Ala	Ser	Val	Gln	Val	Arg	Leu	Leu	Trp	Asp	Val	Leu	Thr	Pro
				95					100					105
Asp	Pro	Asn	Ser	Cys	Pro	Pro	Leu	Tyr	Val	Leu	Trp	Arg	Val	His
				110					115					120
Ser	Gln	Ile	Pro	Gln	Arg	Val	Val	Trp	Pro	Gly	Pro	Val	Pro	Ala
				125					130					135
Ser	Leu	Ser	Leu	Ala	Leu	Leu	Glu	Ser	Val	Leu	Arg	His	Val	Gly
				140					145					150
Leu	Asn	Glu	Val	His	Lys	Ala	Val	Gly	Leu	Leu	Leu	Glu	Thr	Leu
				155					160					165
Gly	Pro	Pro	Pro	Thr	Gly	Leu	His	Leu	Gln	Arg	Gly	Ile	Tyr	Arg
				170					175					180
Glu	Ile	Leu	Phe	Leu	Thr	Met	Ala	Ala	Leu	Gly	Lys	Asp	His	Val
				185					190					195
Asp	Ile	Val	Ala	Phe	Asp	Lys	Lys	Tyr	Lys	Ser	Ala	Phe	Asn	Lys
				200					205					210
Leu	Ala	Ser	Ser	Met	Gly	Lys	Glu	Glu	Leu	Arg	His	Arg	Arg	Ala
				215					220					225
Gln	Met	Pro	Thr	Pro	Lys	Ala	Ile	Asp	Cys	Arg	Lys	Cys	Phe	Gly
				230					235					240

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Ala Pro Pro Glu Cys
245

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GBLANOT02
- (B) CLONE: 2530650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58 :

Met	Leu	Leu	Pro	Gln	Leu	Cys	Trp	Leu	Pro	Leu	Leu	Ala	Gly	Leu	
				5					10					15	
Leu	Pro	Pro	Val	Pro	Ala	Gln	Lys	Phe	Ser	Ala	Leu	Thr	Phe	Leu	
				20					25					30	
Arg	Val	Asp	Gln	Asp	Lys	Asp	Lys	Asp	Cys	Ser	Leu	Asp	Cys	Ala	
				35					40					45	
Gly	Ser	Pro	Gln	Lys	Pro	Leu	Cys	Ala	Ser	Asp	Gly	Arg	Thr	Phe	
				50					55					60	
Leu	Ser	Arg	Cys	Glu	Phe	Gln	Arg	Ala	Lys	Cys	Lys	Asp	Pro	Gln	
				65					70					75	
Leu	Glu	Ile	Ala	Tyr	Arg	Gly	Asn	Cys	Lys	Asp	Val	Ser	Arg	Cys	
				80					85					90	
Val	Ala	Glu	Arg	Lys	Tyr	Thr	Gln	Glu	Gln	Ala	Arg	Lys	Glu	Phe	
				95					100					105	
Gln	Gln	Val	Phe	Ile	Pro	Glu	Cys	Asn	Asp	Asp	Gly	Thr	Tyr	Ser	
				110					115					120	
Gln	Val	Gln	Cys	His	Ser	Tyr	Thr	Gly	Tyr	Cys	Trp	Cys	Val	Thr	
				125					130					135	
Pro	Asn	Gly	Arg	Pro	Ile	Ser	Gly	Thr	Ala	Val	Ala	His	Lys	Thr	
				140					145					150	
Pro	Arg	Cys	Pro	Gly	Ser	Val	Asn	Glu	Lys	Leu	Pro	Gln	Arg	Glu	
				155					160					165	
Gly	Thr	Gly	Lys	Thr	Asp	Asp	Ala	Ala	Ala	Pro	Ala	Leu	Glu	Thr	
				170					175					180	
Gln	Pro	Gln	Gly	Asp	Glu	Glu	Asp	Ile	Ala	Ser	Arg	Tyr	Pro	Thr	
				185					190					195	
Leu	Trp	Thr	Glu	Gln	Val	Lys	Ser	Arg	Gln	Asn	Lys	Thr	Asn	Lys	
				200					205					210	
Asn	Ser	Val	Ser	Ser	Cys	Asp	Gln	Glu	His	Gln	Ser	Ala	Leu	Glu	
				215					220					225	
Glu	Ala	Lys	Gln	Pro	Lys	Asn	Asp	Asn	Val	Val	Ile	Pro	Glu	Cys	
				230					235					240	
Ala	His	Gly	Gly	Leu	Tyr	Lys	Pro	Val	Gln	Cys	His	Pro	Ser	Thr	
				245					250					255	
Gly	Tyr	Cys	Trp	Cys	Val	Leu	Val	Asp	Thr	Gly	Arg	Pro	Ile	Pro	
				260					265					270	
Gly	Thr	Ser	Thr	Arg	Tyr	Glu	Gln	Pro	Lys	Cys	Asp	Asn	Thr	Gly	
				275					280					285	
Gln	Gly	Pro	Pro	Ser	Gln	Ser	Pro	Gly	Pro	Val	Gln	Gly	Pro	Pro	
				290					295					300	
Ala	Thr	Arg	Leu	Ser	Gly	Cys	Gln	Lys	Ala						

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THYMNOT04
- (B) CLONE: 2652271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59 :

Met	Arg	Pro	Ala	Ala	Leu	Arg	Gly	Ala	Leu	Leu	Gly	Cys	Leu	Cys	5	10	15
Leu	Ala	Leu	Leu	Cys	Leu	Gly	Gly	Ala	Asp	Lys	Arg	Leu	Arg	Asp	20	25	30
Asn	His	Glu	Trp	Lys	Lys	Leu	Ile	Met	Val	Gln	His	Trp	Pro	Glu	35	40	45
Thr	Val	Cys	Glu	Lys	Ile	Gln	Asn	Asp	Cys	Arg	Asp	Pro	Pro	Asp	50	55	60
Tyr	Trp	Thr	Ile	His	Gly	Leu	Trp	Pro	Asp	Lys	Ser	Glu	Gly	Cys	65	70	75
Asn	Arg	Ser	Trp	Pro	Phe	Asn	Leu	Glu	Glu	Ile	Lys	Asp	Leu	Leu	80	85	90
Pro	Glu	Met	Arg	Ala	Tyr	Trp	Pro	Asp	Val	Ile	His	Ser	Phe	Pro	95	100	105
Asn	Arg	Ser	Arg	Phe	Trp	Lys	His	Glu	Trp	Glu	Lys	His	Gly	Thr	110	115	120
Cys	Ala	Ala	Gln	Val	Asp	Ala	Leu	Asn	Ser	Gln	Lys	Lys	Tyr	Phe	125	130	135
Gly	Arg	Ser	Leu	Glu	Leu	Tyr	Arg	Glu	Leu	Asp	Leu	Asn	Ser	Val	140	145	150
Leu	Leu	Lys	Leu	Gly	Ile	Lys	Pro	Ser	Ile	Asn	Tyr	Tyr	Gln	Val	155	160	165
Ala	Asp	Phe	Lys	Asp	Ala	Leu	Ala	Arg	Val	Tyr	Gly	Val	Ile	Pro	170	175	180
Lys	Ile	Gln	Cys	Leu	Pro	Pro	Ser	Gln	Asp	Glu	Glu	Val	Gln	Thr	185	190	195
Ile	Gly	Gln	Ile	Glu	Leu	Cys	Leu	Thr	Lys	Gln	Asp	Gln	Gln	Leu	200	205	210
Gln	Asn	Cys	Thr	Glu	Pro	Gly	Glu	Gln	Pro	Ser	Pro	Lys	Gln	Glu	215	220	225
Val	Trp	Leu	Ala	Asn	Gly	Ala	Ala	Glu	Ser	Arg	Gly	Leu	Arg	Val	230	235	240
Cys	Glu	Asp	Gly	Pro	Val	Phe	Tyr	Pro	Pro	Pro	Lys	Lys	Thr	Lys	245	250	255

His

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: LUNGTUT11
(B) CLONE: 2746976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60 :

Met	Gln	Phe	Met	Leu	Leu	Phe	Ser	Arg	Gln	Gly	Lys	Leu	Arg	Leu			
				5					10					15			
Gln	Lys	Trp	Tyr	Val	Pro	Leu	Ser	Asp	Lys	Glu	Lys	Arg	Lys	Ile			
				20					25					30			
Thr	Arg	Glu	Leu	Val	Gln	Thr	Val	Leu	Ala	Arg	Lys	Pro	Lys	Met			
				35					40					45			
Cys	Ser	Phe	Leu	Glu	Trp	Arg	Asp	Leu	Lys	Ile	Val	Tyr	Lys	Arg			
				50					55					60			
Tyr	Ala	Ser	Leu	Tyr	Phe	Cys	Cys	Ala	Ile	Glu	Asp	Gln	Asp	Asn			
				65					70					75			
Glu	Leu	Ile	Thr	Leu	Glu	Ile	Ile	His	Arg	Tyr	Val	Glu	Leu	Leu			
				80					85					90			
Asp	Lys	Tyr	Phe	Gly	Ser	Val	Cys	Glu	Leu	Asp	Ile	Ile	Phe	Asn			
				95					100					105			
Phe	Glu	Lys	Ala	Tyr	Phe	Ile	Leu	Asp	Glu	Phe	Leu	Leu	Gly	Gly			
				110					115					120			
Glu	Val	Gln	Glu	Thr	Ser	Lys	Lys	Asn	Val	Leu	Lys	Ala	Ile	Glu			
				125					130					135			
Gln	Ala	Asp	Leu	Leu	Gln	Glu	Asp	Ala	Lys	Glu	Ala	Glu	Thr	Pro			
				140					145					150			
Arg	Ser	Val	Leu	Glu	Glu	Ile	Gly	Leu	Thr								
				155					160								

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 341 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: THP1AZS08
(B) CLONE: 2753496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61 :

Met	Lys	Arg	Ala	Leu	Gly	Arg	Arg	Lys	Gly	Val	Trp	Leu	Arg	Leu			
				5					10					15			
Arg	Lys	Ile	Leu	Phe	Cys	Val	Leu	Gly	Leu	Tyr	Ile	Ala	Ile	Pro			
				20					25					30			
Phe	Leu	Ile	Lys	Leu	Cys	Pro	Gly	Ile	Gln	Ala	Lys	Leu	Ile	Phe			
				35					40					45			
Leu	Asn	Phe	Val	Arg	Val	Pro	Tyr	Phe	Ile	Asp	Leu	Lys	Lys	Pro			
				50					55					60			
Gln	Asp	Gln	Gly	Leu	Asn	His	Thr	Cys	Asn	Tyr	Tyr	Leu	Gln	Pro			
				65					70					75			
Glu	Glu	Asp	Val	Thr	Ile	Gly	Val	Trp	His	Thr	Val	Pro	Ala	Val			

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				80					85					90
Trp	Trp	Lys	Asn	Ala	Gln	Gly	Lys	Asp	Gln	Met	Trp	Tyr	Glu	Asp
				95					100					105
Ala	Leu	Ala	Ser	Ser	His	Pro	Ile	Ile	Leu	Tyr	Leu	His	Gly	Asn
				110					115					120
Ala	Gly	Thr	Arg	Gly	Gly	Asp	His	Arg	Val	Glu	Leu	Tyr	Lys	Val
				125					130					135
Leu	Ser	Ser	Leu	Gly	Tyr	His	Val	Val	Thr	Phe	Asp	Tyr	Arg	Gly
				140					145					150
Trp	Gly	Asp	Ser	Val	Gly	Thr	Pro	Ser	Glu	Arg	Gly	Met	Thr	Tyr
				155					160					165
Asp	Ala	Leu	His	Val	Phe	Asp	Trp	Ile	Lys	Ala	Arg	Ser	Gly	Asp
				170					175					180
Asn	Pro	Val	Tyr	Ile	Trp	Gly	His	Ser	Leu	Gly	Thr	Gly	Val	Ala
				185					190					195
Thr	Asn	Leu	Val	Arg	Arg	Leu	Cys	Glu	Arg	Glu	Thr	Pro	Pro	Asp
				200					205					210
Ala	Leu	Ile	Leu	Glu	Ser	Pro	Phe	Thr	Asn	Ile	Arg	Glu	Glu	Ala
				215					220					225
Lys	Ser	His	Pro	Phe	Ser	Val	Ile	Tyr	Arg	Tyr	Phe	Pro	Gly	Phe
				230					235					240
Asp	Trp	Phe	Phe	Leu	Asp	Pro	Ile	Thr	Ser	Ser	Gly	Ile	Lys	Phe
				245					250					255
Ala	Asn	Asp	Glu	Asn	Val	Lys	His	Ile	Ser	Cys	Pro	Leu	Leu	Ile
				260					265					270
Leu	His	Ala	Glu	Asp	Asp	Pro	Val	Val	Pro	Phe	Gln	Leu	Gly	Arg
				275					280					285
Lys	Leu	Tyr	Ser	Ile	Ala	Ala	Pro	Ala	Arg	Ser	Phe	Arg	Asp	Phe
				290					295					300
Lys	Val	Gln	Phe	Val	Pro	Phe	His	Ser	Asp	Leu	Gly	Tyr	Arg	His
				305					310					315
Lys	Tyr	Ile	Tyr	Lys	Ser	Pro	Glu	Leu	Pro	Arg	Ile	Leu	Arg	Glu
				320					325					330
Phe	Leu	Gly	Lys	Ser	Glu	Pro	Glu	His	Gln	His				
				335					340					

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: OVARTUT03
- (B) CLONE: 2781553

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62 :

Met	Ala	Glu	Gly	Glu	Asp	Val	Gly	Trp	Trp	Arg	Ser	Trp	Leu	Gln
				5					10					15
Gln	Ser	Tyr	Gln	Ala	Val	Lys	Glu	Lys	Ser	Ser	Glu	Ala	Leu	Glu
				20					25					30
Phe	Met	Lys	Arg	Asp	Leu	Thr	Glu	Phe	Thr	Gln	Val	Val	Gln	His
				35					40					45
Asp	Thr	Ala	Cys	Thr	Ile	Ala	Ala	Thr	Ala	Ser	Val	Val	Lys	Glu
				50					55					60

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Lys	Leu	Ala	Thr	Glu	Gly	Ser	Ser	Gly	Ala	Thr	Glu	Lys	Met	Lys	65	70	75
Lys	Gly	Leu	Ser	Asp	Phe	Leu	Gly	Val	Ile	Ser	Asp	Thr	Phe	Ala	80	85	90
Pro	Ser	Pro	Asp	Lys	Thr	Ile	Asp	Cys	Asp	Val	Ile	Thr	Leu	Met	95	100	105
Gly	Thr	Pro	Ser	Gly	Thr	Ala	Glu	Pro	Tyr	Asp	Gly	Thr	Lys	Ala	110	115	120
Arg	Leu	Tyr	Ser	Leu	Gln	Ser	Asp	Pro	Ala	Thr	Tyr	Cys	Asn	Glu	125	130	135
Pro	Asp	Gly	Pro	Pro	Glu	Leu	Phe	Asp	Ala	Trp	Leu	Ser	Gln	Phe	140	145	150
Cys	Leu	Glu	Glu	Lys	Lys	Gly	Glu	Ile	Ser	Glu	Leu	Leu	Val	Gly	155	160	165
Ser	Pro	Ser	Ile	Arg	Ala	Leu	Tyr	Thr	Lys	Met	Val	Pro	Ala	Ala	170	175	180
Val	Ser	His	Ser	Glu	Phe	Trp	His	Arg	Tyr	Phe	Tyr	Lys	Val	His	185	190	195
Gln	Leu	Glu	Gln	Glu	Gln	Ala	Arg	Arg	Asp	Ala	Leu	Lys	Gln	Arg	200	205	210
Ala	Glu	Gln	Ser	Ile	Ser	Glu	Glu	Pro	Gly	Trp	Glu	Glu	Glu	Glu	215	220	225
Glu	Glu	Leu	Met	Gly	Ile	Ser	Pro	Ile	Ser	Pro	Lys	Glu	Ala	Lys	230	235	240
Val	Pro	Val	Ala	Lys	Ile	Ser	Thr	Phe	Pro	Glu	Gly	Glu	Pro	Gly	245	250	255
Pro	Gln	Ser	Pro	Cys	Glu	Glu	Asn	Leu	Val	Thr	Ser	Val	Glu	Pro	260	265	270
Pro	Ala	Glu	Val	Thr	Pro	Ser	Glu	Ser	Ser	Glu	Ser	Ile	Ser	Leu	275	280	285
Val	Thr	Gln	Ile	Ala	Asn	Pro	Ala	Thr	Ala	Pro	Glu	Ala	Arg	Val	290	295	300
Leu	Pro	Lys	Asp	Leu	Ser	Gln	Lys	Leu	Leu	Glu	Ala	Ser	Leu	Glu	305	310	315
Glu	Gln	Gly	Leu	Ala	Val	Asp	Val	Gly	Glu	Thr	Gly	Pro	Ser	Pro	320	325	330
Pro	Ile	His	Ser	Lys	Pro	Leu	Thr	Pro	Ala	Gly	His	Thr	Gly	Gly	335	340	345
Pro	Glu	Pro	Arg	Pro	Pro	Ala	Arg	Val	Glu	Thr	Leu	Arg	Glu	Glu	350	355	360
Ala	Pro	Thr	Asp	Leu	Arg	Val	Phe	Glu	Leu	Asn	Ser	Asp	Ser	Gly	365	370	375
Lys	Ser	Thr	Pro	Ser	Asn	Asn	Gly	Lys	Lys	Gly	Ser	Ser	Thr	Asp	380	385	390
Ile	Ser	Glu	Asp	Trp	Glu	Lys	Asp	Phe	Asp	Leu	Asp	Met	Thr	Glu	395	400	405
Glu	Glu	Val	Gln	Met	Ala	Leu	Ser	Lys	Val	Asp	Ala	Ser	Gly	Glu	410	415	420
Leu	Glu	Asp	Val	Glu	Trp	Glu	Asp	Trp	Glu						425	430	

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: ADRETUT06

(B) CLONE: 2821925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63 :

Met	Gly	Pro	Val	Arg	Leu	Gly	Ile	Leu	Leu	Phe	Leu	Phe	Leu	Ala	
				5					10					15	
Val	His	Glu	Ala	Trp	Ala	Gly	Met	Leu	Lys	Glu	Glu	Asp	Asp	Asp	
				20					25					30	
Thr	Glu	Arg	Leu	Pro	Ser	Lys	Cys	Glu	Val	Cys	Lys	Leu	Leu	Ser	
				35					40					45	
Thr	Glu	Leu	Gln	Ala	Glu	Leu	Ser	Arg	Thr	Gly	Arg	Ser	Arg	Glu	
				50					55					60	
Val	Leu	Glu	Leu	Gly	Gln	Val	Leu	Asp	Thr	Gly	Lys	Arg	Lys	Arg	
				65					70					75	
His	Val	Pro	Tyr	Ser	Val	Ser	Glu	Thr	Arg	Leu	Glu	Glu	Ala	Leu	
				80					85					90	
Glu	Asn	Leu	Cys	Glu	Arg	Ile	Leu	Asp	Tyr	Ser	Val	His	Ala	Glu	
				95					100					105	
Arg	Lys	Gly	Ser	Leu	Arg	Tyr	Ala	Lys	Gly	Gln	Ser	Gln	Thr	Met	
				110					115					120	
Ala	Thr	Leu	Lys	Gly	Leu	Val	Gln	Lys	Gly	Val	Lys	Val	Asp	Leu	
				125					130					135	
Gly	Ile	Pro	Leu	Glu	Leu	Leu	Gly								
				140											

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 301 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: UTRSTUT05

(B) CLONE: 2879068

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64 :

Met	Glu	Asp	Met	Asn	Glu	Tyr	Ser	Asn	Ile	Glu	Glu	Phe	Ala	Glu	
				5					10					15	
Gly	Ser	Lys	Ile	Asn	Ala	Ser	Lys	Asn	Gln	Gln	Asp	Asp	Gly	Lys	
				20					25					30	
Met	Phe	Ile	Gly	Gly	Leu	Ser	Trp	Asp	Thr	Ser	Lys	Lys	Asp	Leu	
				35					40					45	
Thr	Glu	Tyr	Leu	Ser	Arg	Phe	Gly	Glu	Val	Val	Asp	Cys	Thr	Ile	
				50					55					60	
Lys	Thr	Asp	Pro	Val	Thr	Gly	Arg	Ser	Arg	Gly	Phe	Gly	Phe	Val	
				65					70					75	
Leu	Phe	Lys	Asp	Ala	Ala	Ser	Val	Asp	Lys	Val	Leu	Glu	Leu	Lys	
				80					85					90	
Glu	His	Lys	Leu	Asp	Gly	Lys	Leu	Ile	Asp	Pro	Lys	Arg	Ala	Lys	
				95					100					105	
Ala	Leu	Lys	Gly	Lys	Glu	Pro	Pro	Lys	Lys	Val	Phe	Val	Gly	Gly	
				110					115					120	
Leu	Ser	Pro	Asp	Thr	Ser	Glu	Glu	Gln	Ile	Lys	Glu	Tyr	Phe	Gly	

Ala Phe Gly Glu	125	Glu Asn Ile Glu	130	Leu Pro Met Asp Thr	135
Thr Asn Glu Arg	140	Arg Gly Phe Cys Phe	145	Ile Thr Tyr Thr Asp	150
Glu Pro Val Lys	155	Lys Leu Leu Glu Ser	160	Arg Tyr His Gln Ile	165
Ser Gly Lys Cys	170	Glu Ile Lys Val Ala	175	Gln Pro Lys Glu Val	180
Arg Gln Gln Gln	185	Gln Gln Lys Gly	190	Arg Gly Ala Ala	195
Gly Gly Arg Gly	200	Gly Thr Arg Gly Arg	205	Gly Arg Gly Gln Gly	210
Asn Trp Asn Gln	215	Gly Phe Asn Asn Tyr	220	Tyr Asp Gln Gly Tyr	225
Asn Tyr Asn Ser	230	Ala Tyr Gly Gly Asp	235	Gln Asn Tyr Ser Gly	240
Gly Gly Tyr Asp	245	Tyr Thr Gly Tyr Asn	250	Tyr Gly Asn Tyr Gly	255
Gly Gln Gly Tyr	260	Ala Asp Tyr Ser Gly	265	Gln Gln Ser Thr Tyr	270
Lys Ala Ser Arg	275	Gly Gly Asn His	280	Gln Asn Asn Tyr Gln	285
Tyr	290		295		300

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SINJNOT02
- (B) CLONE: 2886757

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65 :

Met Gly Glu Pro Gln Gln Val Ser Ala	5	Leu Pro Pro Pro Pro Met	15
Gln Tyr Ile Lys Glu Tyr Thr Asp Glu	10	Asn Ile Gln Glu Gly Leu	20
Ala Pro Lys Pro Pro Pro Pro Ile Lys	25	Asp Ser Tyr Met Met Phe	30
Gly Asn Gln Phe Gln Cys Asp Asp Leu	35	Ile Ile Arg Pro Leu Glu	40
Ser Gln Gly Ile Glu Arg Leu His Pro	45	Met Gln Phe Asp His Lys	50
Lys Glu Leu Arg Lys Leu Asn Met Ser	55	Ile Leu Ile Asn Phe Leu	60
Asp Leu Leu Asp Ile Leu Ile Arg Ser	65	Pro Gly Ser Ile Lys Arg	70
Glu Glu Lys Leu Glu Asp Leu Lys Leu	75	Phe Val His Val His	80
His Leu Ile Asn Glu Tyr Arg Pro His	85	Gln Ala Arg Glu Thr Leu	90
Arg Val Met Met Glu Val Gln Lys Arg	95	Gln Arg Leu Glu Thr Ala	100
	105		110
	115		120
	125		130
	135		140
	145		150

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Glu	Arg	Phe	Gln	Lys	His	Leu	Glu	Arg	Val	Ile	Glu	Met	Ile	Gln
				155					160					165
Asn	Cys	Leu	Ala	Ser	Leu	Pro	Asp	Asp	Leu	Pro	His	Ser	Glu	Ala
				170					175					180
Gly	Met	Arg	Val	Lys	Thr	Glu	Pro	Met	Asp	Ala	Asp	Asp	Ser	Asn
				185					190					195
Asn	Cys	Thr	Gly	Gln	Asn	Glu	His	Gln	Arg	Glu	Asn	Ser	Gly	His
				200					205					210
Arg	Arg	Asp	Gln	Ile	Ile	Glu	Lys	Asp	Ala	Ala	Leu	Cys	Val	Leu
				215					220					225
Ile	Asp	Glu	Met	Asn	Glu	Arg	Pro							
				230										

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SCORNOT04
- (B) CLONE: 2964329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66 :

Met	Ala	Gly	Ala	Gly	Ala	Gly	Ala	Gly	Ala	Arg	Gly	Gly	Ala	Ala
				5					10					15
Ala	Gly	Val	Glu	Ala	Arg	Ala	Arg	Asp	Pro	Pro	Pro	Ala	His	Arg
				20					25					30
Ala	His	Pro	Arg	His	Pro	Arg	Pro	Ala	Ala	Gln	Pro	Ser	Ala	Arg
				35					40					45
Arg	Met	Asp	Gly	Gly	Ser	Gly	Gly	Leu	Gly	Ser	Gly	Asp	Asn	Ala
				50					55					60
Pro	Thr	Thr	Glu	Ala	Leu	Phe	Val	Ala	Leu	Gly	Ala	Gly	Val	Thr
				65					70					75
Ala	Leu	Ser	His	Pro	Leu	Leu	Tyr	Val	Lys	Leu	Leu	Ile	Gln	Val
				80					85					90
Gly	His	Glu	Pro	Met	Pro	Pro	Thr	Leu	Gly	Thr	Asn	Val	Leu	Gly
				95					100					105
Arg	Lys	Val	Leu	Tyr	Leu	Pro	Ser	Phe	Phe	Thr	Tyr	Ala	Lys	Tyr
				110					115					120
Ile	Val	Gln	Val	Asp	Gly	Lys	Ile	Gly	Leu	Phe	Arg	Gly	Leu	Ser
				125					130					135
Pro	Arg	Leu	Met	Ser	Asn	Ala	Leu	Ser	Thr	Val	Thr	Arg	Gly	Ser
				140					145					150
Met	Lys	Lys	Val	Phe	Pro	Pro	Asp	Glu	Ile	Glu	Gln	Val	Ser	Asn
				155					160					165
Lys	Asp	Asp	Met	Lys	Thr	Ser	Leu	Lys	Lys	Val	Val	Lys	Glu	Thr
				170					175					180
Ser	Tyr	Glu	Met	Met	Met	Gln	Cys	Val	Ser	Arg	Met	Leu	Ala	His
				185					190					195
Pro	Leu	His	Val	Ile	Ser	Met	Arg	Cys	Met	Val	Gln	Phe	Val	Gly
				200					205					210
Arg	Glu	Ala	Lys	Tyr	Ser	Gly	Val	Leu	Ser	Ser	Ile	Gly	Lys	Ile
				215					220					225
Phe	Lys	Glu	Glu	Gly	Leu	Leu	Gly	Phe	Phe	Val	Gly	Leu	Ile	Pro

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His	Leu	Leu	Gly	Asp	Val	Val	Phe	Leu	Trp	Gly	Cys	Asn	Leu	Leu	230	235	240
Ala	His	Phe	Ile	Asn	Ala	Tyr	Leu	Val	Asp	Asp	Ser	Phe	Ser	Gln	245	250	255
Ala	Leu	Ala	Ile	Arg	Ser	Tyr	Thr	Lys	Phe	Val	Met	Gly	Ile	Ala	260	265	270
Val	Ser	Met	Leu	Thr	Tyr	Pro	Phe	Leu	Leu	Val	Gly	Asp	Leu	Met	275	280	285
Ala	Val	Asn	Asn	Cys	Gly	Leu	Gln	Ala	Gly	Leu	Pro	Pro	Tyr	Ser	290	295	300
Pro	Val	Phe	Lys	Ser	Trp	Ile	His	Cys	Trp	Lys	Tyr	Leu	Ser	Val	305	310	315
Gln	Gly	Gln	Leu	Phe	Arg	Gly	Ser	Ser	Leu	Leu	Phe	Arg	Arg	Val	320	325	330
Ser	Ser	Gly	Ser	Cys	Phe	Ala	Leu	Glu							335	340	345
															350		

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SCORNOT04
- (B) CLONE: 2965248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67 :

Met	Ala	Ser	Thr	Ile	Ser	Ala	Tyr	Lys	Glu	Lys	Met	Lys	Glu	Leu	5	10	15
Ser	Val	Leu	Ser	Leu	Ile	Cys	Ser	Cys	Phe	Tyr	Thr	Gln	Pro	His	20	25	30
Pro	Asn	Thr	Val	Tyr	Gln	Tyr	Gly	Asp	Met	Glu	Val	Lys	Gln	Leu	35	40	45
Asp	Lys	Arg	Ala	Ser	Gly	Gln	Ser	Phe	Glu	Val	Ile	Leu	Lys	Ser	50	55	60
Pro	Ser	Asp	Leu	Ser	Pro	Glu	Ser	Pro	Met	Leu	Ser	Ser	Pro	Pro	65	70	75
Lys	Lys	Lys	Asp	Thr	Ser	Leu	Glu	Glu	Leu	Gln	Lys	Arg	Leu	Glu	80	85	90
Ala	Ala	Glu	Glu	Arg	Arg	Lys	Thr	Gln	Glu	Ala	Gln	Val	Leu	Lys	95	100	105
Gln	Leu	Ala	Asp	Gly	Ala	Ser	Thr	Ser	Ala	Arg	Cys	Cys	Thr	Arg	110	115	120
Arg	Trp	Arg	Arg	Ile	Thr	Thr	Ser	Ala	Ala	Arg	Arg	Arg	Arg	Ser	125	130	135
Ser	Thr	Thr	Arg	Trp	Ser	Ser	Ala	Arg	Arg	Ser	Ala	Arg	His	Thr	140	145	150
Trp	Pro	His	Cys	Ala	Ser	Gly	Cys	Ala	Arg	Arg	Ser	Cys	Thr	Arg	155	160	165
Pro	Arg	Cys	Ala	Gly	Thr	Arg	Ser	Ser	Glu	Lys	Arg	Cys	Arg	Ala	170	175	180
Lys	Gly	Pro	Gly	Arg	Ala	Ala	Pro	Ile	Leu	Arg	Arg	Asn	Thr	Phe	185	190	195

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Gly	Phe	Trp	Phe	Cys	Phe	Val	His	Leu	Cys	Leu	Asp	Ala	Thr	Phe
				200					205					210
Val	Pro	Pro	Pro	Pro	Pro	Gln	Pro	Pro	Ala	Ser	Cys	Phe	Ser	Ser
				215					220					225
Ala	Leu	Ser	Arg	Pro	Ala	Leu	Ser	Ser	Trp					
				230					235					

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: TLYMNOT06

(B) CLONE: 3000534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68 :

Met	Trp	Ser	Ala	Gly	Arg	Gly	Gly	Ala	Ala	Trp	Pro	Val	Leu	Leu
				5					10					15
Gly	Leu	Leu	Leu	Ala	Leu	Leu	Val	Pro	Gly	Gly	Gly	Ala	Ala	Lys
				20					25					30
Thr	Gly	Ala	Glu	Leu	Val	Thr	Cys	Gly	Ser	Val	Leu	Lys	Leu	Leu
				35					40					45
Asn	Thr	His	His	Arg	Val	Arg	Leu	His	Ser	His	Asp	Ile	Lys	Tyr
				50					55					60
Gly	Ser	Gly	Ser	Gly	Gln	Gln	Ser	Val	Thr	Gly	Val	Glu	Ala	Ser
				65					70					75
Asp	Asp	Ala	Asn	Ser	Tyr	Trp	Arg	Ile	Arg	Gly	Gly	Ser	Glu	Gly
				80					85					90
Gly	Cys	Pro	Arg	Gly	Ser	Pro	Val	Arg	Cys	Gly	Gln	Ala	Val	Arg
				95					100					105
Leu	Thr	His	Val	Leu	Thr	Gly	Lys	Asn	Leu	His	Thr	His	His	Phe
				110					115					120
Pro	Ser	Pro	Leu	Ser	Asn	Asn	Gln	Glu	Val	Ser	Ala	Phe	Gly	Glu
				125					130					135
Asp	Gly	Glu	Gly	Asp	Asp	Leu	Asp	Leu	Trp	Thr	Val	Arg	Cys	Ser
				140					145					150
Gly	Gln	His	Trp	Glu	Arg	Glu	Ala	Ala	Val	Arg	Phe	Gln	His	Val
				155					160					165
Gly	Thr	Ser	Val	Phe	Leu	Ser	Val	Thr	Gly	Glu	Gln	Tyr	Gly	Ser
				170					175					180
Pro	Ile	Arg	Gly	Gln	His	Glu	Val	His	Gly	Met	Pro	Ser	Ala	Asn
				185					190					195
Thr	His	Asn	Thr	Trp	Lys	Ala	Met	Glu	Gly	Ile	Phe	Ile	Lys	Pro
				200					205					210
Ser	Val	Glu	Pro	Ser	Ala	Gly	His	Asp	Glu	Leu				
				215					220					

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 483 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: HEAANOT01
(B) CLONE: 3046870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69 :

Met	Lys	Ala	Phe	His	Thr	Phe	Cys	Val	Val	Leu	Leu	Val	Phe	Gly	
				5					10					15	
Ser	Val	Ser	Glu	Ala	Lys	Phe	Asp	Asp	Phe	Glu	Asp	Glu	Glu	Asp	
				20					25					30	
Ile	Val	Glu	Tyr	Asp	Asn	Asp	Phe	Ala	Glu	Phe	Glu	Asp	Val		
				35				40						45	
Met	Glu	Asp	Ser	Val	Thr	Glu	Ser	Pro	Gln	Arg	Val	Ile	Ile	Thr	
				50					55					60	
Glu	Asp	Asp	Glu	Asp	Glu	Thr	Thr	Val	Glu	Leu	Glu	Gly	Gln	Asp	
				65					70					75	
Glu	Asn	Gln	Glu	Gly	Asp	Phe	Glu	Asp	Ala	Asp	Thr	Gln	Glu	Gly	
				80					85					90	
Asp	Thr	Glu	Ser	Glu	Pro	Tyr	Asp	Asp	Glu	Glu	Phe	Glu	Gly	Tyr	
				95					100					105	
Glu	Asp	Lys	Pro	Asp	Thr	Ser	Ser	Ser	Lys	Asn	Lys	Asp	Pro	Ile	
				110					115					120	
Thr	Ile	Val	Asp	Val	Pro	Ala	His	Leu	Gln	Asn	Ser	Trp	Glu	Ser	
				125					130					135	
Tyr	Tyr	Leu	Glu	Ile	Leu	Met	Val	Thr	Gly	Leu	Leu	Ala	Tyr	Ile	
				140					145					150	
Met	Asn	Tyr	Ile	Ile	Gly	Lys	Asn	Lys	Asn	Ser	Arg	Leu	Ala	Gln	
				155					160					165	
Ala	Trp	Phe	Asn	Thr	His	Arg	Glu	Leu	Leu	Glu	Ser	Asn	Phe	Thr	
				170					175					180	
Leu	Val	Gly	Asp	Asp	Gly	Thr	Asn	Lys	Glu	Ala	Thr	Ser	Thr	Gly	
				185					190					195	
Lys	Leu	Asn	Gln	Glu	Asn	Glu	His	Ile	Tyr	Asn	Leu	Trp	Cys	Ser	
				200					205					210	
Gly	Arg	Val	Cys	Cys	Glu	Gly	Met	Leu	Ile	Gln	Leu	Arg	Phe	Leu	
				215					220					225	
Lys	Arg	Gln	Asp	Leu	Leu	Asn	Val	Leu	Ala	Arg	Met	Met	Arg	Pro	
				230					235					240	
Val	Ser	Asp	Gln	Val	Gln	Ile	Lys	Val	Thr	Met	Asn	Asp	Glu	Asp	
				245					250					255	
Met	Asp	Thr	Tyr	Val	Phe	Ala	Val	Gly	Thr	Arg	Lys	Ala	Leu	Val	
				260					265					270	
Arg	Leu	Gln	Lys	Glu	Met	Gln	Asp	Leu	Ser	Glu	Phe	Cys	Ser	Asp	
				275					280					285	
Lys	Pro	Lys	Ser	Gly	Ala	Lys	Tyr	Gly	Leu	Pro	Asp	Ser	Leu	Ala	
				290					295					300	
Ile	Leu	Ser	Glu	Met	Gly	Glu	Val	Thr	Asp	Gly	Met	Met	Asp	Thr	
				305					310					315	
Lys	Met	Val	His	Phe	Leu	Thr	His	Tyr	Ala	Asp	Lys	Ile	Glu	Ser	
				320					325					330	
Val	His	Phe	Ser	Asp	Gln	Phe	Ser	Gly	Pro	Lys	Ile	Met	Gln	Glu	
				335					340					345	
Glu	Gly	Gln	Pro	Leu	Lys	Leu	Pro	Asp	Thr	Lys	Arg	Thr	Leu	Leu	
				350					355					360	
Phe	Thr	Phe	Asn	Val	Pro	Gly	Ser	Gly	Asn	Thr	Tyr	Pro	Lys	Asp	
				365					370					375	

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Met	Glu	Ala	Leu	Leu	Pro	Leu	Met	Asn	Met	Val	Ile	Tyr	Ser	Ile
				380					385					390
Asp	Lys	Ala	Lys	Lys	Phe	Arg	Leu	Asn	Arg	Glu	Gly	Lys	Gln	Lys
				395					400					405
Ala	Asp	Lys	Asn	Arg	Ala	Arg	Val	Glu	Glu	Asn	Phe	Leu	Lys	Leu
				410					415					420
Thr	His	Val	Gln	Arg	Gln	Glu	Ala	Ala	Gln	Ser	Arg	Arg	Glu	Glu
				425					430					435
Lys	Lys	Arg	Ala	Glu	Lys	Glu	Arg	Ile	Met	Asn	Glu	Glu	Asp	Pro
				440					445					450
Glu	Lys	Gln	Arg	Arg	Leu	Glu	Glu	Ala	Ala	Leu	Arg	Arg	Glu	Gln
				455					460					465
Lys	Lys	Leu	Glu	Lys	Lys	Gln	Met	Lys	Met	Lys	Gln	Ile	Lys	Val
				470					475					480
Lys	Ala	Met												

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PONSAT01
- (B) CLONE: 3057669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70 :

Met	Asp	His	Glu	Asp	Ile	Ser	Glu	Ser	Val	Asp	Ala	Ala	Tyr	Asn
				5					10					15
Leu	Gln	Asp	Ser	Cys	Leu	Thr	Asp	Cys	Asp	Val	Glu	Asp	Gly	Thr
				20					25					30
Met	Asp	Gly	Asn	Asp	Glu	Gly	His	Ser	Phe	Glu	Leu	Cys	Pro	Ser
				35					40					45
Glu	Ala	Ser	Pro	Tyr	Val	Arg	Ser	Arg	Glu	Arg	Thr	Ser	Ser	Ser
				50					55					60
Ile	Val	Phe	Glu	Asp	Ser	Gly	Cys	Asp	Asn	Ala	Ser	Ser	Lys	Glu
				65					70					75
Glu	Pro	Lys	Thr	Asn	Arg	Leu	His	Ile	Gly	Asn	His	Cys	Ala	Asn
				80					85					90
Lys	Leu	Thr	Ala	Phe	Lys	Pro	Thr	Ser	Ser	Lys	Ser	Ser	Ser	Glu
				95					100					105
Ala	Thr	Leu	Ser	Ile	Ser	Pro	Pro	Arg	Pro	Thr	Thr	Leu	Ser	Leu
				110					115					120
Asp	Leu	Thr	Lys	Asn	Thr	Thr	Glu	Lys	Leu	Gln	Pro	Ser	Ser	Pro
				125					130					135
Lys	Val	Tyr	Leu	Tyr	Ile	Gln	Met	Gln	Leu	Cys	Arg	Lys	Glu	Asn
				140					145					150
Leu	Lys	Asp	Trp	Met	Asn	Gly	Arg	Cys	Thr	Ile	Glu	Glu	Arg	Glu
				155					160					165
Arg	Ser	Val	Cys	Leu	His	Ile	Phe	Leu	Gln	Ile	Ala	Glu	Ala	Val
				170					175					180
Glu	Phe	Leu	His	Ser	Lys	Gly	Leu	Met	His	Arg	Asp	Leu	Lys	Pro
				185					190					195
Ser	Asn	Ile	Phe	Phe	Thr	Met	Asp	Asp	Val	Val	Lys	Val	Gly	Asp
				200					205					210
Phe	Gly	Leu	Val	Thr	Ala	Met	Asp	Gln	Asp	Glu	Glu	Glu	Gln	Thr

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Val	Leu	Thr	Pro	Met	Pro	Ala	Tyr	Ala	Arg	His	Thr	Gly	Gln	Val	215	220	225
Gly	Thr	Lys	Leu	Tyr	Met	Ser	Pro	Glu	Gln	Ile	His	Gly	Asn	Ser	230	235	240
Tyr	Ser	His	Lys	Val	Asp	Ile	Phe	Ser	Leu	Gly	Leu	Ile	Leu	Phe	245	250	255
Glu	Leu	Leu	Tyr	Pro	Phe	Ser	Thr	Gln	Met	Glu	Arg	Val	Arg	Thr	260	265	270
Leu	Thr	Asp	Val	Arg	Asn	Leu	Lys	Phe	Pro	Pro	Leu	Phe	Thr	Gln	275	280	285
Lys	Tyr	Pro	Cys	Glu	Tyr	Val	Met	Val	Gln	Asp	Met	Leu	Ser	Pro	290	295	300
Ser	Pro	Met	Glu	Arg	Pro	Glu	Ala	Ile	Asn	Ile	Ile	Glu	Asn	Ala	305	310	315
Val	Phe	Glu	Asp	Leu	Asp	Phe	Pro	Gly	Lys	Thr	Val	Leu	Arg	Gln	320	325	330
Arg	Ser	Arg	Ser	Leu	Ser	Ser	Ser	Gly	Thr	Lys	His	Ser	Arg	Gln	335	340	345
Ser	Asn	Asn	Ser	His	Ser	Pro	Leu	Pro	Ser	Asn					350	355	360
															365	370	

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: HEAONOT03
- (B) CLONE: 3088178

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71 :

Met	Met	Asn	Asn	Arg	Phe	Arg	Lys	Asp	Met	Met	Lys	Asn	Ala	Ser	5	10	15
Glu	Ser	Lys	Leu	Ser	Lys	Asp	Asn	Leu	Lys	Lys	Arg	Leu	Lys	Glu	20	25	30
Glu	Phe	Gln	His	Ala	Met	Gly	Gly	Val	Pro	Ala	Trp	Ala	Glu	Thr	35	40	45
Thr	Lys	Arg	Lys	Thr	Ser	Ser	Asp	Asp	Glu	Ser	Glu	Glu	Asp	Glu	50	55	60
Asp	Asp	Leu	Leu	Gln	Arg	Thr	Gly	Asn	Phe	Ile	Ser	Thr	Ser	Thr	65	70	75
Ser	Leu	Pro	Arg	Gly	Ile	Leu	Lys	Met	Lys	Asn	Cys	Gln	His	Ala	80	85	90
Asn	Ala	Glu	Arg	Pro	Thr	Val	Ala	Arg	Ile	Ser	Ser	Val	Gln	Phe	95	100	105
His	Pro	Gly	Ala	Gln	Ile	Val	Met	Val	Ala	Gly	Leu	Asp	Asn	Ala	110	115	120
Val	Ser	Leu	Phe	Gln	Val	Asp	Gly	Lys	Thr	Asn	Pro	Lys	Ile	Gln	125	130	135
Ser	Ile	Tyr	Leu	Glu	Arg	Phe	Pro	Ile	Phe	Lys	Ala	Cys	Phe	Ser	140	145	150
Ala	Asn	Gly	Glu	Glu	Val	Leu	Ala	Thr	Ser	Thr	His	Ser	Lys	Val	155	160	165

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Leu	Tyr	Val	Tyr	Asp	Met	Leu	Ala	Gly	Lys	Leu	Ile	Pro	Val	His
				170					175					180
Gln	Val	Arg	Gly	Leu	Lys	Glu	Lys	Ile	Val	Arg	Ser	Phe	Glu	Val
				185					190					195
Ser	Pro	Asp	Gly	Ser	Phe	Leu	Leu	Ile	Asn	Gly	Ile	Ala	Gly	Tyr
				200					205					210
Leu	His	Leu	Leu	Ala	Met	Lys	Thr	Lys	Glu	Leu	Ile	Gly	Ser	Met
				215					220					225
Lys	Ile	Asn	Gly	Arg	Val	Ala	Ala	Ser	Thr	Phe	Ser	Ser	Asp	Ser
				230					235					240
Lys	Lys	Val	Tyr	Ala	Ser	Ser	Gly	Asp	Gly	Glu	Val	Tyr	Val	Trp
				245					250					255
Asp	Val	Asn	Ser	Arg	Lys	Cys	Leu	Asn	Arg	Phe	Val	Asp	Glu	Gly
				260					265					270
Ser	Leu	Tyr	Gly	Leu	Ser	Ile	Ala	Thr	Ser	Arg	Asn	Gly	Gln	Tyr
				275					280					285
Val	Ala	Cys	Gly	Ser	Asn	Cys	Gly	Val	Val	Asn	Ile	Tyr	Asn	Gln
				290					295					300
Asp	Ser	Cys	Leu	Gln	Glu	Thr	Asn	Pro	Lys	Pro	Ile	Lys	Ala	Ile
				305					310					315
Met	Asn	Leu	Val	Thr	Gly	Val	Thr	Ser	Leu	Thr	Phe	Asn	Pro	Thr
				320					325					330
Thr	Glu	Ile	Leu	Ala	Ile	Ala	Ser	Glu	Lys	Met	Lys	Glu	Ala	Val
				335					340					345
Arg	Leu	Val	His	Leu	Pro	Ser	Cys	Thr	Val	Phe	Ser	Asn	Phe	Pro
				350					355					360
Val	Ile	Lys	Asn	Lys	Asn	Ile	Ser	His	Val	His	Thr	Met	Asp	Phe
				365					370					375
Ser	Pro	Arg	Ser	Gly	Tyr	Phe	Ala	Leu	Gly	Asn	Glu	Lys	Gly	Lys
				380					385					390
Ala	Leu	Met	Tyr	Arg	Leu	His	His	Tyr	Ser	Asp	Phe			
				395					400					

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 640 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTNOT19
- (B) CLONE: 3094321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72 :

Met	Ala	Leu	Ser	Arg	Gly	Leu	Pro	Arg	Glu	Leu	Ala	Glu	Ala	Val
				5					10					15
Ala	Gly	Gly	Arg	Val	Leu	Val	Val	Gly	Ala	Gly	Gly	Ile	Gly	Cys
				20					25					30
Glu	Leu	Leu	Lys	Asn	Leu	Val	Leu	Thr	Gly	Phe	Ser	His	Ile	Asp
				35					40					45
Leu	Ile	Asp	Leu	Asp	Thr	Ile	Asp	Val	Ser	Asn	Leu	Asn	Arg	Gln
				50					55					60
Phe	Leu	Phe	Gln	Lys	Lys	His	Val	Gly	Arg	Ser	Lys	Ala	Gln	Val
				65					70					75
Ala	Lys	Glu	Ser	Val	Leu	Gln	Phe	Tyr	Pro	Lys	Ala	Asn	Ile	Val

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				80					85				90	
Ala	Tyr	His	Asp	Ser	Ile	Met	Asn	Pro	Asp	Tyr	Asn	Val	Glu	Phe
				95					100					105
Phe	Arg	Gln	Phe	Ile	Leu	Val	Met	Asn	Ala	Leu	Asp	Asn	Arg	Ala
				110					115					120
Ala	Arg	Asn	His	Val	Asn	Arg	Met	Cys	Leu	Ala	Ala	Asp	Val	Pro
				125					130					135
Leu	Ile	Glu	Ser	Gly	Thr	Ala	Gly	Tyr	Leu	Gly	Gln	Val	Thr	Thr
				140					145					150
Ile	Lys	Lys	Gly	Val	Thr	Glu	Cys	Tyr	Glu	Cys	His	Pro	Lys	Pro
				155					160					165
Thr	Gln	Arg	Thr	Phe	Pro	Gly	Cys	Thr	Ile	Arg	Asn	Thr	Pro	Ser
				170					175					180
Glu	Pro	Ile	His	Cys	Ile	Val	Trp	Ala	Lys	Tyr	Leu	Phe	Asn	Gln
				185					190					195
Leu	Phe	Gly	Glu	Glu	Asp	Ala	Asp	Gln	Glu	Val	Ser	Pro	Asp	Arg
				200					205					210
Ala	Asp	Pro	Glu	Ala	Ala	Trp	Glu	Pro	Thr	Glu	Ala	Glu	Ala	Arg
				215					220					225
Ala	Arg	Ala	Ser	Asn	Glu	Asp	Gly	Asp	Ile	Lys	Arg	Ile	Ser	Thr
				230					235					240
Lys	Glu	Trp	Ala	Lys	Ser	Thr	Gly	Tyr	Asp	Pro	Val	Lys	Leu	Phe
				245					250					255
Thr	Lys	Leu	Phe	Lys	Asp	Asp	Ile	Arg	Tyr	Leu	Leu	Thr	Met	Asp
				260					265					270
Lys	Leu	Trp	Arg	Lys	Arg	Lys	Pro	Pro	Val	Pro	Leu	Asp	Trp	Ala
				275					280					285
Glu	Val	Gln	Ser	Gln	Gly	Glu	Glu	Thr	Asn	Ala	Ser	Asp	Gln	Gln
				290					295					300
Asn	Glu	Pro	Gln	Leu	Gly	Leu	Lys	Asp	Gln	Gln	Val	Leu	Asp	Val
				305					310					315
Lys	Ser	Tyr	Ala	Arg	Leu	Phe	Ser	Lys	Ser	Ile	Glu	Thr	Leu	Arg
				320					325					330
Val	His	Leu	Ala	Glu	Lys	Gly	Asp	Gly	Ala	Glu	Leu	Ile	Trp	Asp
				335					340					345
Lys	Asp	Asp	Pro	Ser	Ala	Met	Asp	Phe	Val	Thr	Ser	Ala	Ala	Asn
				350					355					360
Leu	Arg	Met	His	Ile	Phe	Ser	Met	Asn	Met	Lys	Ser	Arg	Phe	Asp
				365					370					375
Ile	Lys	Ser	Met	Ala	Gly	Asn	Ile	Ile	Pro	Ala	Ile	Ala	Thr	Thr
				380					385					390
Asn	Ala	Val	Ile	Ala	Gly	Leu	Ile	Val	Leu	Glu	Gly	Leu	Lys	Ile
				395					400					405
Leu	Ser	Gly	Lys	Ile	Asp	Gln	Cys	Arg	Thr	Ile	Phe	Leu	Asn	Lys
				410					415					420
Gln	Pro	Asn	Pro	Arg	Lys	Lys	Leu	Leu	Val	Pro	Cys	Ala	Leu	Asp
				425					430					435
Pro	Pro	Asn	Pro	Asn	Cys	Tyr	Val	Cys	Ala	Ser	Lys	Pro	Glu	Val
				440					445					450
Thr	Val	Arg	Leu	Asn	Val	His	Lys	Val	Thr	Val	Leu	Thr	Leu	Gln
				455					460					465
Asp	Lys	Ile	Val	Lys	Glu	Lys	Phe	Ala	Met	Val	Ala	Pro	Asp	Val
				470					475					480
Gln	Ile	Glu	Asp	Gly	Lys	Gly	Thr	Ile	Leu	Ile	Ser	Ser	Glu	Glu
				485					490					495
Gly	Glu	Thr	Glu	Ala	Asn	Asn	His	Lys	Lys	Leu	Ser	Glu	Phe	Gly
				500					505					510
Ile	Arg	Asn	Gly	Ser	Arg	Leu	Gln	Ala	Asp	Asp	Phe	Leu	Gln	Asp
				515					520					525
Tyr	Thr	Leu	Leu	Ile	Asn	Ile	Leu	His	Ser	Glu	Asp	Leu	Gly	Lys
				530					535					540

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Asp	Val	Glu	Phe	Glu	Val	Val	Gly	Asp	Ala	Pro	Glu	Lys	Val	Gly	
				545					550					555	
Pro	Lys	Gln	Ala	Glu	Asp	Ala	Ala	Lys	Ser	Ile	Thr	Asn	Gly	Ser	
				560					565					570	
Asp	Asp	Gly	Ala	Gln	Pro	Ser	Thr	Ser	Thr	Ala	Gln	Glu	Gln	Asp	
				575					580					585	
Asp	Val	Leu	Ile	Val	Asp	Ser	Asp	Glu	Glu	Asp	Ser	Ser	Asn	Asn	
				590					595					600	
Ala	Asp	Val	Ser	Glu	Glu	Glu	Arg	Ser	Arg	Lys	Arg	Lys	Leu	Asp	
				605					610					615	
Glu	Lys	Glu	Asn	Leu	Ser	Ala	Lys	Arg	Ser	Arg	Ile	Glu	Gln	Lys	
				620					625					630	
Glu	Glu	Leu	Asp	Asp	Val	Ile	Ala	Leu	Asp						
				635					640						

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGTUT13
- (B) CLONE: 3115936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73 :

Met	Asp	Lys	Ile	Leu	Asn	Val	Glu	Glu	Thr	Tyr	Leu	Thr	Val	Leu	
				5					10					15	
Val	Lys	Ile	Gly	Pro	Gly	Phe	His	Thr	Arg	Glu	Cys	Phe	Leu	Leu	
				20					25					30	
Lys	Ser	Ile	Leu	Cys	Phe	Ser	Pro	Ser	Tyr	Arg	Met	Ser	Glu	Gly	
				35					40					45	
Asp	Ser	Val	Gly	Glu	Ser	Val	His	Gly	Lys	Pro	Ser	Val	Val	Tyr	
				50					55					60	
Arg	Phe	Phe	Thr	Arg	Leu	Gly	Gln	Ile	Tyr	Gln	Ser	Trp	Leu	Asp	
				65					70					75	
Lys	Ser	Thr	Pro	Tyr	Thr	Ala	Val	Arg	Trp	Val	Val	Thr	Leu	Gly	
				80					85					90	
Leu	Ser	Phe	Val	Tyr	Met	Ile	Arg	Val	Tyr	Leu	Leu	Gln	Gly	Trp	
				95					100					105	
Tyr	Ile	Val	Thr	Tyr	Ala	Leu	Gly	Ile	Tyr	His	Leu	Asn	Leu	Phe	
				110					115					120	
Ile	Ala	Phe	Leu	Ser	Pro	Lys	Val	Asp	Pro	Ser	Leu	Met	Glu	Asp	
				125					130					135	
Ser	Asp	Asp	Gly	Pro	Ser	Leu	Pro	Thr	Lys	Gln	Asn	Glu	Glu	Phe	
				140					145					150	
Arg	Pro	Phe	Ile	Arg	Arg	Leu	Pro	Glu	Phe	Lys	Phe	Trp	His	Ala	
				155					160					165	
Ala	Thr	Lys	Gly	Ile	Leu	Val	Ala	Met	Val	Cys	Thr	Phe	Phe	Asp	
				170					175					180	
Ala	Phe	Asn	Val	Pro	Val	Phe	Trp	Pro	Ile	Leu	Val	Met	Tyr	Phe	
				185					190					195	
Ile	Met	Leu	Phe	Cys	Ile	Thr	Met	Lys	Arg	Gln	Ile	Lys	His	Met	
				200					205					210	
Ile	Lys	Tyr	Arg	Tyr	Ile	Pro	Phe	Thr	His	Gly	Lys	Arg	Arg	Tyr	

	215		220	225
Arg Gly Lys Glu	Asp Ala Gly Lys Ala	Phe Ala Ser		
	230	235		

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGTUT13
 (B) CLONE: 3116522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74 :

Met	Asp	Ala	Arg	Trp	Trp	Ala	Val	Val	Val	Leu	Ala	Ala	Phe	Pro	5	10	15
Ser	Leu	Gly	Ala	Gly	Gly	Glu	Thr	Pro	Glu	Ala	Pro	Pro	Glu	Ser	20	25	30
Trp	Thr	Gln	Leu	Trp	Phe	Phe	Arg	Phe	Val	Val	Asn	Ala	Ala	Gly	35	40	45
Tyr	Ala	Ser	Phe	Met	Val	Pro	Gly	Tyr	Leu	Leu	Val	Gln	Tyr	Phe	50	55	60
Arg	Arg	Lys	Asn	Tyr	Leu	Glu	Thr	Gly	Arg	Gly	Leu	Cys	Phe	Pro	65	70	75
Leu	Val	Lys	Ala	Cys	Val	Phe	Gly	Asn	Glu	Pro	Lys	Ala	Ser	Asp	80	85	90
Glu	Val	Pro	Leu	Ala	Pro	Arg	Thr	Glu	Ala	Ala	Glu	Thr	Thr	Pro	95	100	105
Met	Trp	Gln	Ala	Leu	Lys	Leu	Leu	Phe	Cys	Ala	Thr	Gly	Leu	Gln	110	115	120
Val	Ser	Tyr	Leu	Thr	Trp	Gly	Val	Leu	Gln	Glu	Arg	Val	Met	Thr	125	130	135
Arg	Ser	Tyr	Gly	Ala	Thr	Ala	Thr	Ser	Pro	Gly	Glu	Arg	Phe	Thr	140	145	150
Asp	Ser	Gln	Phe	Leu	Val	Leu	Met	Asn	Arg	Val	Leu	Ala	Leu	Ile	155	160	165
Val	Ala	Gly	Leu	Ser	Cys	Val	Leu	Cys	Lys	Gln	Pro	Arg	His	Gly	170	175	180
Ala	Pro	Met	Tyr	Arg	Tyr	Ser	Phe	Ala	Ser	Leu	Ser	Asn	Val	Leu	185	190	195
Ser	Ser	Trp	Cys	Gln	Tyr	Glu	Ala	Leu	Lys	Phe	Val	Ser	Phe	Pro	200	205	210
Thr	Gln	Val	Leu	Ala	Lys	Ala	Ser	Lys	Val	Ile	Pro	Val	Met	Leu	215	220	225
Met	Gly	Lys	Leu	Val	Ser	Arg	Arg	Ser	Tyr	Glu	His	Trp	Glu	Tyr	230	235	240
Leu	Thr	Ala	Thr	Leu	Ile	Ser	Ile	Gly	Val	Ser	Met	Phe	Leu	Leu	245	250	255
Ser	Ser	Gly	Pro	Glu	Pro	Arg	Ser	Ser	Pro	Ala	Thr	Thr	Leu	Ser	260	265	270
Gly	Leu	Ile	Leu	Leu	Ala	Gly	Tyr	Ile	Ala	Phe	Asp	Ser	Phe	Thr	275	280	285
Ser	Asn	Trp	Gln	Asp	Ala	Leu	Phe	Ala	Tyr	Lys	Met	Ser	Ser	Val	290	295	300

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Gln	Met	Met	Phe	Gly	Val	Asn	Phe	Phe	Ser	Cys	Leu	Phe	Thr	Val
				305					310					315
Gly	Ser	Leu	Leu	Glu	Gln	Gly	Ala	Leu	Leu	Glu	Gly	Thr	Arg	Phe
				320					325					330
Met	Gly	Arg	His	Ser	Glu	Phe	Ala	Ala	His	Ala	Leu	Leu	Leu	Ser
				335					340					345
Ile	Cys	Ser	Ala	Cys	Gly	Gln	Leu	Phe	Ile	Phe	Tyr	Thr	Ile	Gly
				350					355					360
Gln	Phe	Gly	Ala	Ala	Val	Phe	Thr	Ile	Ile	Met	Thr	Leu	Arg	Gln
				365					370					375
Ala	Phe	Ala	Ile	Leu	Leu	Ser	Cys	Leu	Leu	Tyr	Gly	His	Thr	Val
				380					385					390
Thr	Val	Val	Gly	Gly	Leu	Gly	Val	Ala	Val	Val	Phe	Ala	Ala	Leu
				395					400					405
Leu	Leu	Arg	Val	Tyr	Ala	Arg	Gly	Arg	Leu	Lys	Gln	Arg	Gly	Lys
				410					415					420
Lys	Ala	Val	Pro	Val	Glu	Ser	Pro	Val	Gln	Lys	Val			
				425					430					

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGTUT13
- (B) CLONE: 3117184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75 :

Met	Ser	Phe	Pro	Pro	His	Leu	Asn	Arg	Pro	Pro	Met	Gly	Ile	Pro
				5					10					15
Ala	Leu	Pro	Pro	Gly	Thr	Pro	Pro	Pro	Gln	Phe	Pro	Gly	Phe	Pro
				20					25					30
Pro	Pro	Val	Pro	Pro	Gly	Thr	Pro	Met	Ile	Pro	Val	Pro	Met	Ser
				35					40					45
Ile	Met	Ala	Pro	Ala	Pro	Thr	Val	Leu	Val	Pro	Thr	Val	Ser	Met
				50					55					60
Val	Gly	Lys	His	Leu	Gly	Ala	Arg	Lys	Asp	His	Pro	Gly	Leu	Lys
				65					70					75
Ala	Lys	Glu	Asn	Asp	Glu	Asn	Cys	Gly	Pro	Thr	Thr	Thr	Val	Phe
				80					85					90
Val	Gly	Asn	Ile	Ser	Glu	Lys	Ala	Ser	Asp	Met	Leu	Ile	Arg	Gln
				95					100					105
Leu	Leu	Ala	Lys	Cys	Gly	Leu	Val	Leu	Ser	Trp	Lys	Arg	Val	Gln
				110					115					120
Gly	Ala	Ser	Gly	Lys	Leu	Gln	Ala	Phe	Gly	Phe	Cys	Glu	Tyr	Lys
				125					130					135
Glu	Pro	Glu	Ser	Thr	Leu	Arg	Ala	Leu	Arg	Leu	Leu	His	Asp	Leu
				140					145					150
Gln	Ile	Gly	Glu	Lys	Lys	Leu	Leu	Val	Lys	Val	Asp	Ala	Lys	Thr
				155					160					165
Lys	Ala	Gln	Leu	Asp	Glu	Trp	Lys	Ala	Lys	Lys	Lys	Ala	Ser	Asn
				170					175					180
Gly	Asn	Ala	Arg	Pro	Glu	Thr	Val	Thr	Asn	Asp	Asp	Glu	Glu	Ala

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Leu Asp Glu Glu Thr	185	Lys Arg Arg Asp	190	Gln Met Ile Lys Gly	195
	200		205		210
Ile Glu Val Leu Ile	215	Arg Glu Tyr Ser	220	Ser Glu Leu Asn Ala	225
Ser Gln Glu Ser Asp	230	Ser His Pro Arg	235	Lys Lys Lys Lys Glu	240
Lys Glu Asp Ile Phe	245	Gly Arg Phe Gln	250	Trp Ala His	

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LNODNOT05
- (B) CLONE: 3125156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76 :

Met Gly Pro Gln Ala	5	Ala Pro Leu Thr	10	Ile Arg Gly Pro Ser	15
Ala Gly Gln Ser Thr	20	Pro Ser Pro His	25	Leu Val Pro Ser Pro	30
Pro Ser Pro Gly Pro	35	Gly Pro Val Pro	40	Pro Arg Pro Pro Ala	45
Glu Pro Pro Pro Cys	50	Leu Arg Arg Gly	55	Ala Ala Ala Asp Leu	60
Leu Ser Ser Ser Pro	65	Glu Ser Gln His	70	Gly Gly Thr Gln Ser	75
Gly Gly Gly Gln Pro	80	Leu Leu Gln Pro	85	Thr Lys Val Asp Ala	90
Glu Gly Arg Arg Pro	95	Gln Ala Leu Arg	100	Leu Ile Glu Arg Asp	105
Tyr Glu His Pro Glu	110	Arg Leu Arg Gln	115	Leu Gln Gln Glu Leu	120
Ala Phe Arg Gly Gln	125	Leu Gly Asp Val	130	Gly Ala Leu Asp Thr	135
Trp Arg Glu Leu Gln	140	Asp Ala Gln Glu	145	His Asp Ala Arg Gly	150
Ser Ile Ala Ile Ala	155	Arg Cys Tyr Ser	160	Leu Lys Asn Arg His	165
Asp Val Met Pro Tyr	170	Asp Ser Asn Arg	175	Val Val Leu Arg Ser	180
Lys Asp Asp Tyr Ile	185	Asn Ala Ser Cys	190	Val Glu Gly Leu Ser	195
Tyr Cys Pro Pro Leu	200	Val Ala Thr Gln	205	Ala Pro Leu Pro Gly	210
Ala Ala Asp Phe Trp	215	Leu Met Val His	220	Glu Gln Lys Val Ser	225
Ile Val Met Leu Val	230	Ser Glu Ala Glu	235	Met Glu Lys Gln Lys	240
Ala Arg Tyr Phe Pro	245	Thr Glu Arg Gly	250	Gln Pro Met Val His	255

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Ala	Leu	Ser	Leu	Ala	Leu	Ser	Ser	Val	Arg	Ser	Thr	Glu	Thr	His
				260					265					270
Val	Glu	Arg	Val	Leu	Ser	Leu	Gln	Phe	Arg	Asp	Gln	Ser	Leu	Lys
				275					280					285
Arg	Ser	Leu	Val	His	Leu	His	Phe	Pro	Thr	Trp	Pro	Glu	Leu	Gly
				290					295					300
Leu	Pro	Asp	Ser	Pro	Ser	Asn	Leu	Leu	Arg	Phe	Ile	Gln	Glu	Val
				305					310					315
His	Ala	His	Tyr	Leu	His	Gln	Arg	Pro	Leu	His	Thr	Pro	Ile	Ile
				320					325					330
Val	His	Cys	Ser	Ser	Gly	Val	Gly	Arg	Thr	Gly	Ala	Phe	Ala	Leu
				335					340					345
Leu	Tyr	Ala	Ala	Val	Gln	Glu	Val	Glu	Ala	Gly	Asn	Gly	Ile	Pro
				350					355					360
Glu	Leu	Pro	Gln	Leu	Val	Arg	Arg	Met	Arg	Gln	Gln	Arg	Lys	His
				365					370					375
Met	Leu	Gln	Glu	Lys	Leu	His	Leu	Arg	Phe	Cys	Tyr	Glu	Ala	Val
				380					385					390
Val	Arg	His	Val	Glu	Gln	Val	Leu	Gln	Arg	His	Gly	Val	Pro	Pro
				395					400					405
Pro	Cys	Lys	Pro	Leu	Ala	Ser	Ala	Ser	Ile	Ser	Gln	Lys	Asn	His
				410					415					420
Leu	Pro	Gln	Asp	Ser	Gln	Asp	Leu	Val	Leu	Gly	Gly	Asp	Val	Pro
				425					430					435
Ile	Ser	Ser	Ile	Gln	Ala	Thr	Ile	Ala	Lys	Leu	Ser	Ile	Arg	Pro
				440					445					450
Pro	Gly	Gly	Leu	Glu	Ser	Pro	Val	Ala	Ser	Leu	Pro	Gly	Pro	Ala
				455					460					465
Glu	Pro	Pro	Gly	Leu	Pro	Pro	Ala	Ser	Leu	Pro	Glu	Ser	Thr	Pro
				470					475					480
Ile	Pro	Ser	Ser	Ser	Gln	Thr	Pro	Phe	Pro	Pro	His	Tyr	Leu	Arg
				485					490					495
Leu	Pro	Ser	Leu	Arg	Arg	Ser	Arg	Gln	Cys	Leu	Lys	Pro	Pro	Ala
				500					505					510
Arg	Gly	Pro	Pro	Pro	Pro	Pro	Trp	Asn	Cys	Trp	Pro	Pro		
				515					520					

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGTUT12
- (B) CLONE: 3129120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77 :

Met	Gly	Leu	Leu	Ser	Asp	Pro	Val	Arg	Arg	Arg	Ala	Leu	Ala	Arg
				5					10					15
Leu	Val	Leu	Arg	Leu	Asn	Ala	Pro	Leu	Cys	Val	Leu	Ser	Tyr	Val
				20					25					30
Ala	Gly	Ile	Ala	Trp	Phe	Leu	Ala	Leu	Val	Phe	Pro	Pro	Leu	Thr
				35					40					45
Gln	Arg	Thr	Tyr	Met	Ser	Glu	Asn	Ala	Met	Gly	Ser	Thr	Met	Val
				50					55					60

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Glu	Glu	Gln	Phe	Ala	Gly	Gly	Asp	Arg	Ala	Arg	Ala	Phe	Ala	Arg	65	70	75
Asp	Phe	Ala	Ala	His	Arg	Lys	Lys	Ser	Gly	Ala	Leu	Pro	Val	Ala	80	85	90
Trp	Leu	Glu	Arg	Thr	Met	Arg	Ser	Val	Gly	Leu	Glu	Val	Tyr	Thr	95	100	105
Gln	Ser	Phe	Ser	Arg	Lys	Leu	Pro	Phe	Pro	Asp	Glu	Thr	His	Glu	110	115	120
Arg	Tyr	Met	Val	Ser	Gly	Thr	Asn	Val	Tyr	Gly	Ile	Leu	Arg	Ala	125	130	135
Pro	Arg	Ala	Ala	Ser	Thr	Glu	Ser	Leu	Val	Leu	Thr	Val	Pro	Cys	140	145	150
Gly	Ser	Asp	Ser	Thr	Asn	Ser	Gln	Ala	Val	Gly	Leu	Leu	Leu	Ala	155	160	165
Leu	Ala	Ala	His	Phe	Arg	Gly	Gln	Ile	Tyr	Trp	Ala	Lys	Asp	Ile	170	175	180
Val	Phe	Leu	Val	Thr	Glu	His	Asp	Leu	Leu	Gly	Thr	Glu	Ala	Trp	185	190	195
Leu	Glu	Ala	Tyr	His	Asp	Val	Asn	Val	Thr	Gly	Met	Gln	Ser	Ser	200	205	210
Pro	Leu	Gln	Gly	Arg	Ala	Gly	Ala	Ile	Gln	Ala	Ala	Val	Ala	Leu	215	220	225
Glu	Leu	Ser	Ser	Asp	Val	Val	Thr	Ser	Leu	Asp	Val	Ala	Val	Glu	230	235	240
Gly	Leu	Asn	Gly	Gln	Leu	Pro	Asn	Leu	Asp	Leu	Leu	Asn	Leu	Phe	245	250	255
Gln	Thr	Phe	Cys	Gln	Lys	Gly	Gly	Leu	Leu	Cys	Thr	Leu	Gln	Gly	260	265	270
Lys	Leu	Gln	Pro	Glu	Asp	Trp	Thr	Ser	Leu	Asp	Gly	Pro	Leu	Gln	275	280	285
Gly	Leu	Gln	Thr	Leu	Leu	Leu	Met	Val	Leu	Arg	Gln	Ala	Ser	Gly	290	295	300
Arg	Pro	His	Gly	Ser	His	Gly	Leu	Phe	Leu	Arg	Tyr	Arg	Val	Glu	305	310	315
Ala	Leu	Thr	Leu	Arg	Gly	Ile	Asn	Ser	Phe	Arg	Gln	Tyr	Lys	Tyr	320	325	330
Asp	Leu	Val	Ala	Val	Gly	Lys	Ala	Leu	Glu	Gly	Met	Phe	Arg	Lys	335	340	345
Leu	Asn	His	Leu	Leu	Glu	Arg	Leu	His	Gln	Ser	Phe	Phe	Leu	Tyr	350	355	360
Leu	Leu	Pro	Gly	Leu	Ser	Arg	Phe	Val	Ser	Ile	Gly	Leu	Tyr	Met	365	370	375
Pro	Ala	Val	Gly	Phe	Leu	Leu	Leu	Val	Leu	Gly	Leu	Lys	Ala	Leu	380	385	390
Glu	Leu	Trp	Met	Gln	Leu	His	Glu	Ala	Gly	Met	Gly	Leu	Glu	Glu	395	400	405
Pro	Gly	Gly	Ala	Pro	Gly	Pro	Ser	Val	Pro	Leu	Pro	Pro	Ser	Gln	410	415	420
Gly	Val	Gly	Leu	Ala	Ser	Leu	Val	Ala	Pro	Leu	Leu	Ile	Ser	Gln	425	430	435
Ala	Met	Gly	Leu	Ala	Leu	Tyr	Val	Leu	Pro	Val	Leu	Gly	Gln	His	440	445	450
Val	Ala	Thr	Gln	His	Phe	Pro	Val	Ala	Glu	Ala	Glu	Ala	Val	Val	455	460	465
Leu	Thr	Leu	Leu	Ala	Ile	Tyr	Ala	Ala	Gly	Leu	Ala	Leu	Pro	His	470	475	480
Asn	Thr	His	Arg	Val	Val	Ser	Thr	Gln	Ala	Pro	Asp	Arg	Gly	Trp	485	490	495
Met	Ala	Leu	Lys	Leu	Val	Ala	Leu	Ile	Tyr	Leu	Ala	Leu	Gln	Leu	500	505	510
Gly	Cys	Ile	Ala	Leu	Thr	Asn	Phe	Ser	Leu	Gly	Phe	Leu	Leu	Ala			

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Thr Thr Met Val	515	Pro Thr Ala Ala Leu	520	Ala Lys Pro His Gly	525
Arg Thr Leu Tyr	530	Ala Ala Leu Leu Val	535	Leu Thr Ser Pro Ala	540
Thr Leu Leu Gly	545	Ser Leu Phe Leu Trp	550	Arg Glu Leu Gln Glu	555
Pro Leu Ser Leu	560	Ala Glu Gly Trp Gln	565	Leu Phe Leu Ala Ala	570
Ala Gln Gly Val	575	Leu Glu His His Thr	580	Tyr Gly Ala Leu Leu	585
Pro Leu Leu Ser	590	Leu Gly Leu Tyr Pro	595	Cys Trp Leu Leu Phe	600
Asn Val Leu Phe	605	Trp Lys	610		615
	620				

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: HEARNOT01
- (B) CLONE: 305841

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78 :

CCCTCGAGAA GATGGCGGCG ACTCTGGGAC CCCTTGGGTC GTGGCAGCAG TGGCGGCGAT 60
GTTTGTCTGGC TCGGGATGGG TCCAGGATGT TACTCCTTCT TCTTTTGTG GGGTCTGGGC 120
AGGGGCCACA GCAAGTCGGG GCGGGTCAAA CGTTCGAGTA CTTGAAACGG GAGCACTCGC 180
TGTCGAAGCC CTACCAGGGT GTGGGCACAG GCAGTTCCTC ACTGTGGAAT CTGATGGGCA 240
ATGCCATGGT GATGACCCAG TATATCCGCC TTACCCCAAGA TATGCAAAGT AAACAGGGTG 300
CCTTGTGGAA CCGGGTGCCA TGTTTCCTGA GAGACTGGGA GTTGCAGGTG CACTTCAAAA 360
TCCATGGACA AGGAAAGAAG AATCTGCATG GGGATGGCTT GGCAATCTGG TACACAAAGG 420
ATCGGATGCA GCCAGGGCCT GTGTTTGGAA ACATGGACAA ATTTGTGGGG CTGGGAGTAT 480
TTGTAGACAC CTACCCCAAT GAGGAGAAGC AGCAAGAGCG GGTATTCCCC TACATCTCAG 540
CCATGGTGAA CAACGGCTCC CTCAGCTATG ATCATGAGCG GGATGGGCGG CCTACAGAGC 600
TGGGAGGCTG CACAGCCATT GTCCGCAATC TTCATTACGA CACCTTCCTG GTGATTCTGCT 660
ACGTCAAGAG GCATTTGACG ATAATGATGG ATATTGATGG CAAGCATGAG TGGAGGGACT 720
GCATTGAAGT GCCCGGAGTC CGCCTGCCCC GCGGCTACTA CTTCCGCACC TCCTCCATCA 780
CTGGGGATCT CTCAGATAAT CATGATGTCA TTTCCTTGAA GTTGTGTTGAA CTGACAGTGG 840

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AGAGAACCCC AGAAGAGGAA AAGCTCCATC GAGATGTGTT CTTGCCCTCA GTGGACAATA 900
TGAAGCTGCC TGAGATGACA GCTCCACTGC CGCCCCTGAG TGGCCTGGCC CTCTTCCTCA 960
TCGTCTTTTT CTCCCTGGTG TTTTCTGTAT TTGCCATAGT CATTGGTATC ATACTCTACA 1020
ACAAATGGCA GGAACAGAGC CGAAAGCGCT TCTACTGAGC CCTCCTGCTG CCACCACTTT 1080
TGTGACTGTC ACCCATGAGG TATGGAAGGA GCAGGCACTG GCCTGAGCAT GCAGCCTGGA 1140
GAGTGTTCCT GTCTCTAGCA GCTGGTTGGG GACTATATTC TGTCACCTGA GTTTTGAATG 1200
CAGGGACCCC GCATTCCCAT GGTGTGTCAT GGGGACATCT AACTCTGGTC TGGGAAGCCA 1260
CCCACCCCAG GGCAATGCTG CTGTGATGTG CCTTCCCTG CAGTCCTTCC ATGTGGGAGC 1320
AGAGGTGTGA AGAGAATTTA CGTGGTTGTG ATGCCAAAAT CACAGAACAG AATTTTCATAG 1380
CCCAGGCTGC CGTGTGTTTT GACTCAGAAG GCCCTTCTAC TTCAGTTTTG AATCCACAAA 1440
GAATTAAAAA CTGGTAACAC CACAGGCTTT CTGACCATCC ATTCGTTGGG TTTTGCATTT 1500
GACCCAACCC TCTGCCTACC TGAGGAGCTT TCTTTGAAAA CCAGGATGGA AACTTCTTCC 1560
CTGCCTTACC TTCCTTTCAC TCCATTCAAT GTCCTCTCTG TGTGCAACCT GAGCTGGGAA 1620
AGGCATTTGG ATGCCTCTCT GTTGGGGCCT GGGGCTGCAG AACACACCTG CGTTTCACTG 1680
GCCTTCATTA GGTGGCCCTA GGGAGATGGC TTTCTGCTTT GGATCACTGT TCCCTAGCAT 1740
GGGTCTTGGG TCTATTGGCA TGTCCATGGC CTTCCCAATC AAGTCTCTTC AGGCCCTCAG 1800
TGAAGTTTGG CTAAAGGTTG GTGTAAAAAT CAAGAGAAGC CTGGAAGACA TCATGGATGC 1860
CATGGATTAG CTGTGCAACT GACCAGCTCC AGGTTTGATC AAACCAAAG CAACATTTGT 1920
CATGTGGTCT GACCATGTGG AGATGTTTCT GGACTTGCTA GAGCCTGCTT AGCTGCATGT 1980
TTTGTAGTTA CGATTTTTGG AATCCCACTT TGAGTGCTGA AAGTGTAAGG AAGCTTTCTT 2040
CTTACACCTT GGGCTTGGAT ATTGCCAGA GAAGAAATTT GGCTTTTTTT TTCTTAATGG 2100
ACAAGAGACA GTTGCTGTTC TCATGTTCCA AGTCTGAGAG CAACAGACCC TCATCATCTG 2160
TGCCTGGAAG AGTTCACTGT CATTGAGCAG CACAGCCTGA GTGCTGGCCT CTGTCAACCC 2220
TTATTCCACT GCCTTATTTG ACAAGGGGTT ACATGCTGCT CACCTTACTG CCCTGGGATT 2280
AAATCAGTTA CAGGCCAGAG TCTCCTTGGA GGGCCTGGAA CTCTGAGTCC TCCTATGAAC 2340
CTCTGTA 2347

(2) INFORMATION FOR SEQ ID NO: 79:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1529 base pairs
(B) TYPE: nucleic acid

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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: EOSIHET02
(B) CLONE: 322866

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79 :

CCCACGCGTC CGCCAGCCTT GTCTCGGCCA CCTCAAGGAT AATCACTAAA TTCTGCCGAA 60
AGGACTGAGG AACGGTGCCT GGAAAAGGGC AAGAATATCA CGGCATGGGC ATGAGTAGCT 120
TGAAACTGCT GAAGTATGTC CTGTTTTTCT TCAACTTGCT CTTTGGATC TGTGGCTGCT 180
GCATTTTGGG CTTTGGGATC TACCTGCTGA TCCACAACAA CTTGGAGTG CTCTTCATA 240
ACCTGCCCTC CCTCACGCTG GGCAATGTGT TTGTCATCGT GGGCTCTATT ATCATGGTAG 300
TTGCCTTCCT GGGCTGCATG GGCTCTATCA AGGAAAACAA GTGTCTGCTT ATGTCGTTCT 360
TCATCCTGCT GCTGATTATC CTCCTTGCTG AGGTGACCTT GGCCATCCTG CTCTTTGTAT 420
ATGAACAGAA GCTGAATGAG TATGTGGCTA AGGGTCTGAC CGACAGCATC CACCGTTACC 480
ACTCAGACAA TAGCACCAAG GCAGCGTGGG ACTCCATCCA GTCATTTCTG CAGTGTTGTG 540
GTATAAATGG CACGAGTGAT TTGGACAGTG GCTCACCAGC ATCTTGCCCC TCAGATCGAA 600
AAGTGAGGG GTGCTATGCG AAAGAAGACT TTGGTTTCAT TCAATTTCTT GTATATCGGA 660
ATCATCACCA TCTGTGTATG TGTGATTGAG GTGTTGGGGG ATGTCCTTTG CACTGACCCT 720
GAACTGCCAG ATTGACAAAA CCAGCCAGAC CATAGGGGCTA TGATCTGCAG TAGTTCTGTG 780
GTGAAGAGAC TTGTTTCATC TCCGGAAATG CAAAACCATT TATAGCATGA AGCCCTACAT 840
GATCACTGCA GGATGATCCT CCTCCCATCC TTTCCCTTTT TAGGTCCCTG TCTTATACAA 900
CCAGAGAAAGT GGGTGTTGGC CAGGCACATC CCATCTCAGG CAGCAAGACA ATCTTTCACT 960
CACTGACGGC AGCAGCCATG TCTCTCAAAG TGGTGAAACT AATATCTGAG CATCTTTTAG 1020
ACAAGAGAGG CAAAGACAAA CTGGATTTAA TGGCCCAACA TCAAAGGGTG AACCCAGGAT 1080
ATGAATTTTT GCATCTTCCC ATTGTGCAAT TAGTCTCCAG CCTCTAAATA ATGCCAGTC 1140
TTCTCCCCAA AGTCAAGCAA GAGACTAGTT GAAGGGAGTT CTGGGGCCAG GCTCACTGGA 1200
CCATTGTCAC AACCTCTGT TTCTCTTTGA CTAAGTGCCC TGGCTACAGG AATTACACAG 1260
TTCTCTTTCT CCAAAGGGCA AGATCTCATT TCAATTTCTT TATTAGAGGG CTTATTGAT 1320
GTGTTCTAAG TCTTTCAGA AAAAACTAT CCAGTGATTT ATATCCTGAT TTCAACCAGT 1380
CACTTAGCTG ATAATCACAG TAAGAAGACT TCTGGTATTA TCTCTCTATC AGATAAGATT 1440
TTGTTAATGT ACTATTTTAC TCTTCAATAA ATAAACAGT TTATTATCTC AAAAAAAAAA 1500
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1529

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BEPINOT01
- (B) CLONE: 546656

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80 :

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GCATCCCCGC TTCCGGGTTA GGCCGTTCTT GCGCGCCCCC TCCTCTCCTC CCTTCGGACC 60
CATAGATCTC AGGCTCGGCT CCGCGCCCGC CGCAGCCCAC TGTTGACCCG GCCCGTACTG 120
CGGCCCCCGTG GCCACCATGT CCCTGCACGG CAAACGGAAG GAGATCTACA AGTATGAAGC 180
GCCCTGGACA GTCTACGCGA TGAAGTGGAG TGTGCGGCCC GATAAGCGCT TTCGCTTGGC 240
GCTGGGCAGC TTCGTGGAGG AGTACAACAA CAAGGTTTCT CTTGTTGGTT TAGATGAGGA 300
GAGTTCAGAG TTTATTTGCA GAAACACCTT TGACCACCCA TACCCACCA CAAAGCTCAT 360
GTGGATCCCT GACACAAAAG GCGTCTATCC AGACCTACTG GCAACAAGCG GTGACTATCT 420
CCGTGTGTGG AGGGTTGGTG AAACAGAGAC CAGGCTGGAG TGTGCTGCTAA ACAATAATAA 480
GAACTCTGAT TTCTGTGCTC CCCTGACCTC CTTTGACTGG AATGAGGTGG ATCCTTATCT 540
TTTAGGTACC TCAAGCATTG ATACGACATG CACCATCTGG GGGCTGGAGA CAGGGCAGGT 600
GTTAGGGCGA GTGAATCTCG TGTCTGGCCA CGTGAAGACC CAGCTGATCG CCCATGACAA 660
AGAGGTCTAT GATATTGCAT TTAGCCGGGC CGGGGGTGGC AGGGACATGT TTGCTCTGT 720
GGGTGCTGAT GGCTCGGTGC GGATGTTTGA CCTCCGCCAT CTAGAACACA GCACCATCAT 780
TTACGAAGAC CCACAGCATC ACCCACTGCT TCGCCTCTGC TGGAACAAGC AGGACCCTAA 840
CTACCTGGCC ACCATGGCCA TGGATGGAAT GGAGGTGGTG ATTCTAGATG TCCGGGTTCC 900
CTGCACACCT GTCGCCAGGT TAAACAACCA TCGAGCATGT GTCAATGGCA TTGCTTGGGC 960
CCCACATTCA TCCTGCCACA TCTGCACTGC AGCGGATGAC CACCAGGCTC TCATCTGGGA 1020
CATCCAGCAA ATGCCCCGAG CCATTGAGGA CCCTATCCTG GCCTACACAG CTGAAGGAGA 1080
GATCAACAAT GTGCAGTGGG CATCAACTCA GCGCGACTGG ATCGCCATCT GCTACAACAA 1140
CTGCCTGGAG AACTCAGAG TGTAGTGTG GTGGCGCTGT GCCACGAGG CAGGGGCTTT 1200
TGTATTTCTT GCCTCTGCCC CACCCCCAAA GTAAGAAGAA ACATGTTTCC AGTGGCCAGT 1260
ATGTCTTTCA TTGCTTTGCA CCCACTGTTA CCAGAAGCTG CTCTAGGAGT TCCTGGCCAG 1320

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TCACCCCATC GCCCTCTGTG GCAGACTCAG TGCTGTGTGG CGCCTCCTCA GCCCAGGGCT 1380
GAGTTTTAAG ATTTTCTCTC CTTTCCTCTT CTCCTTTGGT TCCTCAATTA AAAAATGTGT 1440
GTATATTTGT TTGTCAGGCG TTGTGTTGAG GAGCAGTTCA CGCACTGGCT GTGTCTATTC 1500
CTCTGCCCAG GTGTCTCTGT TTGCTGCCCCA AGGCAGCAGT TCATGTCTCG TCCATGTCCA 1560
TGTTCTGTGT AGCACTTACG TGGGAACAAA TACCAATTTG TCTTTTCTCC TAGTATCAGT 1620
GTGTTTAACA AATTTTAACT TTGTATATTT GTTATCTATC AGGCTAATTT TTTTATGAAA 1680
AGAATTTTAC TCTCCTGCTT CATTTCTTTG TCTTATAGTC CTCCCTCTTT GCACCTTCTT 1740
CTCTTCCCTC AGTGCCTGGA GCTGGTACTG GGCCCTGGG CCCCATGAGC AGTTTGCCTT 1800
CTTGAGTCAC TGCCTGTGTA GTACATACCT GACCGGGAGT CCAAACCACC TTGGTGCTCT 1860
GAAGTCCACT GACTCATCAC ACCTTTCTTA GCCTGGCTCC TCTCAAGGGC ATTCTGGGCT 1920
TGTAACAGA CATAGGAAGC CTCTGTTTAC CCTGAAGCAC CACTGTCCAG CCCATTGGTT 1980
CCCACTGGCA GCATGGTAGA GCTGAGAGAA ACAGGCTCTC AGGGTACCTG ACTTGAGGGG 2040
AATCGTTTCA TGAAGCTGAA CTTCAAGCAT ATTTCCAGTA CATTCTTTCA GAGTCTGTTT 2100
TTCCATCCAA ATATAAGCCC CAGGCCATTC CACTTAGTGT CTTTTCAATG ATAGGCAAGA 2160
ATGATATCTG AGTTGAACTT CGGTGCTTCT GTTGTTTGAG TTTACTGTGC CTGGTGGTAT 2220
ATTGGGCATT CTTTGGATTG AGTGTTCTGA GGTGAGAGAG TCTTCCCGAG GCATCCTGTC 2280
TGTGCTTCCA ACCCTGAACA AGACCTTACA TGAGAGATGG ACTGATGGAC TGCGGCAATC 2340
CTGGGCTGTC AAGTGGATAG ATAGTTAAAA AGCATTATAC TGTGGGTAAT GAAAAGGGAG 2400
GAAAAAAAAA GAAGGAAAAG GAATTATAGA CCCCCAGGGT CAGCCAGTTA AGAGCTCTAC 2460
CCACACCTGT CAACCCCTCT CTCCCCCAGT TTAGGTTCTG AGCAGTATTG GACTTGTAGC 2520
CTGCAGTTGT CTTTTGACTT GCAGGCCGCA GGTGTCTTTC TGTTATGTGA ATGAGTTCCA 2580
TGGAGGGGCA TATGTGTGAT TCCACCGTTA GATGAGCCCT TGGGGCAGGC AGTTTGGGAT 2640
GTGCTCTTGG GGGAAAGTTG GCTGTTTCCT TCGCTCTGC TCCTACCCGA AGGTTTTTAA 2700
GTCCCTCTGA ATTGCTCATC TGAGATTAGT AGAGTAGCAG GCCTGAAGGA TGATGGTTTT 2760
GTCCTCTTTG GTTCTCACCT GCTTGAGAAG TAAAACAGTA ACTTTGTTCT TCTGGGCCCT 2820
TAAGCTTTTT TGGTTAAGTC TTCCTTTTCA GAAGTAGATG TCATTATATG CCAAAGTCT 2880
AGCTCTTTGC TTTACCATAC AGGGACCTGT CCCAAAGAAA AAGGCTCTTT TTTTAGCCAG 2940
CATATTTCCC CTTCTACCCT TTTACTTTGT TGTTCTGATT TTAGGACTCT GGCTGGCCAT 3000
GTGCTTGTGG TTGCCTCTCC TGCATTTGCC ACTGGATTTG CACTGCATCG TTTGGAGATA 3060
CAAAGCGAGC AGTTCTTGGT CAGAACCCTC CTCTGCTTTT CATTGTGTTT GATAATGGTT 3120
ACTGGGTCCT TCTCTCAAGG GTAGCAAGGC CAAGCTGATG GCTGCTTGTT TAGGAGGCCA 3180

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TCAGTTCCTT CCTGTGGAGA AGGGTCTGAA ATGGAAGTCA GTGGTAGAAG GGGCTGGTCT 3240
GCTGGGCAGG GCTTACATCC ACTGAGTTCT AAGATTCCTT TCCTGATCTG CACCTACGCC 3300
TGGTCTGTAT GGTGGAATTT GTCAGCTGGA ACTCAGAAAC AACAACTGA AAAAAAATA 3360
ATAATTAGAA CATATTTGCA TAAGATAGCT ATTTACTCTG GAAACCAACA ACTTTTGAGA 3420
TTTCCCTTGC CCTGTGGACG CCCAGCTCCT GTCATCCTTC CTTAGGTCCT GCAGTACAGT 3480
CTTCCCCTGA ATGCCACCGG GGACCCAGGG GGA CTCCACC CCCCTAAGCA AGCACACACA 3540
TACTCACAGT TGATGAGTTG CTGGTCTTTG AGTCCCAGCT CTCTTACCCT CCCTTTACTC 3600
CACCAGCCCG ACGACCCATG ACTGAGGAGG GGATTTCTAC AGTCTCAGGA TTTAGAAAGT 3660
CTGTAAGCCA TCCATGCTCC AGAAAGCACC GATCTGTTGT AGTTGCAAAA ACAACTCTGT 3720
AATTTGTTGA GGTTCCTCAA CTGACAGCCA GCGAGACTGG GTGGGAGGCC CTGGATCTGT 3780
TCTCCCTGAC TGC GGGAGGA GCAGCCACTA GGACTTTAGC AGGAAGCCCA CATGGAGGCT 3840
CCGCCAGGCT GTGGCCAGC TGGTGATGGC CCTTTTGCTC CTGGCAGCCT GAGGCACAGC 3900
TGCCTGTATT GTCCTCATCT GTTCTGACTG AAGGATGGAG GTGCTGAATA AATTAGGCCT 3960
CAGGCCTCTA CCACCAGAGA GCTGGAGAAT GGGTCCACGT CATTCAAGGA CCTGAATTTT 4020
TTATGCTCAG GAGCATTGGA ATCCTCTTCT TCCAGGGAGG AATTAGCCTG CAAGGTTAGG 4080
ACTTGAAGAG GGAAGGTATT TAATAACTGG GCGAGGATGG GTGTGGTGGC TCACACCTGT 4140
AATCCCAGCA TTTTGGGAGG CTGAGGTGGC CAGATCCCAA GGTCAGAAGA TCGAGACCAT 4200
CCTGGCTAAC ATGGTGAAAC CCCATCTCTA CTAAAAATAC AAAAAAAAT TAGCCGGGGG 4260
TGGTGGCGGG TACCTGTAGT CCTAGCTACT TGGGAGGCTG AGGCAGGAGA ATGGCGTGAA 4320
CCTGGGAGGT GGAGCTTGCA GTGAGCCAAG ATCGTCCACT CACTGCAGCC TGGCGACAGA 4380
GCAAGCG 4387

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SYNORAT03
- (B) CLONE: 693453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81 :

GCCTGAGCGG GAAGCATTGG CGTCCGAGCG ACTTCTAGGA GCCTGGGGTT CGGCGCTATG 60

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GAGGAGCTCG ATGGCGAGCC AACAGTCACT TTGATTCCAG GCGTGAATTC CAAGAAGAAC 120
CAAATGTATT TTGACTGGGG TCCAGGGGAG ATGCTGGTAT GTGAAACCTC CTTCAACAAA 180
AAAGAAAAAT CAGAGATGGT GCCAAGTTGC CCCTTTATCT ATATCATCCG TAAGGATGTA 240
GATGTTTACT CTCAAATCTT GAGAAAACCTC TTCAATGAAT CCCATGGAAT CTTTCTGGGC 300
CTCCAGAGAA TTGACGAAGA GTTGAAGTGA AAATCCAGAA AATCTCAATT GGTTCGAGTG 360
AGTAAAAACT ACCGATCAGT CATCAGAGCA TGTATGGAGG AAATGCACCA GGTTCGAATT 420
GCTGCTAAAG ATCCAGCCAA TGGCCGCCAG TTCAGCAGCC AGGTCTCCAT TTTGTGAGCA 480
ATGGAGCTCA TCTGGAACCT GTGTGAGATT CTTTTTATTG AAGTGGCCCC AGCTGGCCCT 540
CTCCTCCTCC ATCTCCTTGA CTGGGTCCGG CTCCATGTGT GCGAGGTGGA CAGTTTGTCTG 600
GCAGATGTTT TGGGCAGTGA GAATCCAAGC AAACATGACA GCTTCTGGAA CTTGGTGACC 660
ATCTTGGTGC TGCAGGGCCG GCTGGATGAG GCGGACAGA TGCTCTCCAA GGAAGCCGAT 720
GCCAGCCCCG CCTCTGCAGG CATATGCCGA ATCATGGGGG ACCTGATGAG GACAATGCCC 780
ATTCTTAGTC CTGGGAACAC CCAGACACTG ACAGAGCTGG AGCTGAAGTG GCAGCACTGG 840
CACGAGGAAT GTGAGCGGTA CCTCCAGGAC AGCACATTCG CCACCAGCCC TCACCTGGAG 900
TCTCTCTTGA AGATTATGCT GGGAGACGAA GCTGCCTTGT TAGAGCAGAA GGAACCTCTG 960
AGTAATTGGT ATCATTTTCT AGTGAAGCTG CTCTTGTACT CCAATCCCAC AGTAAAACCC 1020
ATTGATCTGC ACTACTATGC CCAGTCCAGC CTGGACCTGT TTCTGGGAGG TGAGAGCAGC 1080
CCAGAACCCC TGGACAACAT CTTGTTGGCA GCCTTTGAGT TTGACATCCA TCAAGTAATC 1140
AAAGAGTGCA GCATCGCCCT GAGCAACTGG TGGTTTGTGG CCCACCTGAC AGACCTGCTG 1200
GACCACTGCA AGCTCCTCCA GTCACACAAC CTCTATTTCT GTTCCAACAT GAGAGAGTTC 1260
CTCCTGCTGG AGTACGCCTC GGGACTGTTT GCTCATCCCA GCCTGTGGCA GCTGGGGGTC 1320
GATTACTTTG ATTACTGCCC CGAGCTGGGC CGAGTCTCCC TGGAGCTGCA CATTGAGCGG 1380
ATACCTCTGA ACACCGAGCA GAAAGCCCTG AAGGTGCTGC GGATCTGTGA GCAGCGGCAG 1440
ATGACTGAAC AAGTTCGCAG CATTTGTAAG ATCTTAGCCA TGAAAGCCGT CCGCAACAAT 1500
CGCCTGGGTT CTGCCCTCTC TTGGAGCATC CGTGCTAAGG ATGCCGCCTT TGCCACGCTC 1560
GTGTCAGACA GGTTCCTCAG GGATTACTGT GAGCGAGGCT GCTTTTCTGA TTTGGATCTC 1620
ATTGACAACC TGGGGCCAGC CATGATGCTC AGTGACCGAC TGACATTCCT GGGAAAGTAT 1680
CGCGAGTTCC ACCGTATGTA CGGGGAGAAG CGTTTTGCCG ACGCAGCTTC TCTCCTTCTG 1740
TCCTTGATGA CGTCTCGGAT TGCCCCTCGG TCTTTCTGGA TGAATCTGCT GACAGATGCC 1800
TTGCCCTTTT TGGAACAGAA ACAGGTGATT TTCTCAGCAG AACAGACTTA TGAGTTGATG 1860
CGGTGTCTGG AGGACTTGAC GTCAAGAAGA CCTGTGCATG GAGAATCTGA TACCGAGCAG 1920

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CTCCAGGATG ATGACATAGA GACCACCAAG GTGGAAATGC TGAGACTTTC TCTGGCACGA 1980
AATCTTGCTC GGGCAATTAT AAGAGAAGGC TCACTGGAAG GTTCCTGAGA ACTGCTTCAA 2040
TGTGGTATCT TTGTATGGCA ATGTATATAG ATTTTTTAAA AGAATAAATG TTGTTTGCAA 2100
AAAAAAAAAA AAAAAAA 2117

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAITUT03
- (B) CLONE: 866885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82 :

GGCGGGCGGA GTCTGCAGGA TGGCACCGGA CCCCTGGTTC TCCACATACG ATTCTACTTG 60
TCAAATTGCC CAAGAAATTG CTGAGAAAAT TCAACAACGA AATCAATATG AAAGAAAAGG 120
TGAAAAGGCA CCAAAGCTTA CCGTGACAAT CAGAGCTTTG TTGCAGAACC TGAAGGAAAA 180
GATCGCCCTT TTGAAGGACT TATTGCTAAG AGCTGTGTCA ACACATCAGA TAACACAGCT 240
TGAAGGGGAC CGAAGACAGA ACCTCTTGGA TGATCTTGTA ACTCGAGAGA GACTACTTCT 300
GGCATCCTTT AAGAATGAGG GTGCCGAACC AGATCTAATC AGGTCCAGCC TGATGAGTGA 360
AGAGGCTAAG CGAGGAGCAC CCAACCCTTG GCTCTTTGAG GAGCCAGAGG AGACCAGAGG 420
CTTGGGTTTT GATGAAATCC GGCAACAGCA GCAGAAAATT ATCCAAGAAC AGGATGCAGG 480
CCTTGATGCC CTTTCCTCTA TCATAAGTCG CCAAAAACAA ATGGGGCAGG AAATTGGGAA 540
TGAATTGGAT GAACAAAATG AGATAATTGA CGACCTTGCC AACCTAGTGG AGAACACAGA 600
TGAAAACTT CGCAATGAAA CCAGGCGGGT AAACATGGTG GACAGAAAGT CAGCCTCTTG 660
TGGGATGATC ATGGTGATTT TACTGCTGCT TGTGGCTATC GTGGTTGTTG CAGTCTGGCC 720
GACCAACTGA TGGCAGTAAA GAGACCACCA GCAGTGACAC CTGGCAATGA CAGATGCAAG 780
CCCAACACCC TTTTGGTACG CAAACCTGC TCTCAATAAA TTCCCCCAA GCTCTGAAAA 840
AAAAAA 846

(2) INFORMATION FOR SEQ ID NO: 83:

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1011 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
(A) LIBRARY: LUNGNOT03
(B) CLONE: 1242271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83 :

GAAAGAGATA ACTGGAAGTT CCTTGATTCA GAAAACAGAT TCAGATGAAG AAGTTGCAAT 60
GCTGTTGGAC ACAGTCCAGA AAGTATTTCA GAAAATGTTG GAATGTATTG CACGGAGCTT 120
CAGGAAGCAG CCGGAAGAAG GCCTGCGGCT GCTTTATTCT GTTCAGAGGC CTCTTCATGA 180
GTTCACTACT GCTGTTCACT CTCGGCACAC AGACACCCCT GTGCACCGGG GTGTAATTTT 240
TACTCTGATC GCTGGGCTTG TGGTTGAGAT AAGTCACCAG CTACGGAAGG TTTCTGACGT 300
AGAAGAGCTT ACCCCTCCAG AGCATCTTTC TGATCTTCCA CCATTTTCAA GGTGTTTAAAT 360
AGGAATAATA ATAAAGTCTT CGAATGTGGT CAGGTCATTT TTGGATGAAT TAAAGGCATG 420
TGTGGCTTCT AATGATATTG AAGGCATTGT GTGCCTCACG GCTGCTGTGC ATATTATCCT 480
GGTTATTAAT GCAGGTAAAC ATAAAAGCTC AAAAGTGAGG GAGGTTGCAG CCACTGTTCA 540
CAGAAAACTA AAGACATTCA TGGAAATTAC TTTGGAAGAG GATAGCATTG AAAGATTTCT 600
CTATGAATCA TCATCAAGAA CTCTGGGAGA ACTTTTGAAT TCATAACCAA GCCAACATCT 660
CCAGACATGT AAAAATAGGG AAAAGTGATT CAAATTGAAA TGCCTGTGTA TTTTCCTATT 720
GTTTTTAATG TTAATAACCC ATATAATAGG GAAAGGGTGG GATTTTTTTT TGGGAATGTG 780
GGAAGGTGGG GGTATGAG GAGATAACTC AAAACTTCTT CAATTTTGCC TAGTGCCTGC 840
GTAAATAATA TATTTAATAT AAAGGACTCC AGGTATGAAT GGTGTAGAAA TCCATGATTC 900
CAAGAAAAAA CACTTTTCTA GCAAACCTGG TTGTTTTTAA AATGACTTTT ATATATGTAA 960
TATTGCTTGG AACTATGAG TAATAAGCA ATGACAACAT CAAAAAAA A 1011

(2) INFORMATION FOR SEQ ID NO: 84:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2478 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
(A) LIBRARY: LUNGFET03
(B) CLONE: 1255027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84 :

CCCACGCGTC CGCCACGCG TCCGCAGCGC TGTGTTTGCG AGCGGGAGCG AGGGGCGCCG 60
 GCTGGGGTGT GTGCTCCTGA GCTCTTCAGA AACCAGGCTG CTTTCAGGAA CATTGCTGTG 120
 GATTCCCAGC TTTCAGACAA CACATGACTA AGACAGATGA GACCACTCTA GTTGCCTCAT 180
 GGGAAACTCG GGAAAAGACT GCAAAAACAA CATTGTTTCT CCCTTTGGAA TTCTGGAGTT 240
 ATAAGGCAGA GGTCCCCCAT CTTCCCGAAC TGGCCTATTC CGCTAGAAGC AAGATGGCTG 300
 AACTCAATAC TCATGTGAAT GTCAAGGAAA AGATCTATGC AGTTAGATCA GTTGTTCCCA 360
 ACAAAGCAA TAATGAAATA GTCCTGGTGC TCCAACAGTT TGATTTTAAT GTGGATAAAG 420
 CCGTGCAAGC CTTTGTGGAT GGCAGTGCAA TTCAAGTTCT AAAAGAATGG AATATGACAG 480
 GCAAAAAGAA GAACAATAAA AGAAAAGAA GCAAGTCCAA GCAGCATCAA GGCAACAAAG 540
 ATGCTAAAGA CAAGGTGGAG AGGCCTGAGG CAGGGCCCCT GCAGCCGCAG CCACCACAGA 600
 TTCAAAACGG CCCCATGAAT GGCTGCGAGA AGGACAGCTC GTCCACAGAT TCTGCTAACG 660
 AAAAACCAGC CTTTATCCCT CGTGAGAAAA AGATCTCGAT ACTTGAGGAA CCTTCAAAGG 720
 CACTTCGTGG GGTACAGAA GGCAACAGAC TACTGCAACA GAACTATCC TTAGATGGGA 780
 ACCCCAAACC TATACATGGA ACAACAGAGA GGTGAGATGG CCTACAGTGG TCAGCTGAGC 840
 AGCCTTGTA CCAGCAAG CCTAAGGCAA AAACATCTCC TGTTAAGTCC AATACCCCTG 900
 CAGCTCATCT TGAAATAAAG CCAGATGAGT TGGCAAAGAA AAGAGGCCCA AATATTGAGA 960
 AATCAGTGAA GGATTTGCAA CGCTGCACCG TTTCTCTAAC TAGATATCGC GTCATGATTA 1020
 AGGAAGAAGT GGATAGTTCC GTGAAGAAGA TCAAAGCTGC CTTTGCTGAA TTACACAACT 1080
 GCATCATTGA CAAAGAAGTT TCATTAATGG CAGAAATGGA TAAAGTTAAA GAAGAAGCCA 1140
 TGGAAATCCT GACTGCTCGT CAGAAGAAAG CAGAAGAACT AAAGAGACTC ACTGACCTTG 1200
 CCAGTCAGAT GGCAGAGATG CAGCTGGCCG AACTCAGGGC AGAAATTAAG CACTTTGTCA 1260
 GCGAGCGTAA ATATGACGAG GAGCTCGGGA AAGCTGCCCCG GTTTTCCTGT GACATCGAAC 1320
 AGCTGAAGGC CCAAATCATG CTCTGCGGAG AAATTACACA TCCAAAGAAC AACTATTCCCT 1380
 CAAGAACTCC CTGCAGCTCC CTGCTGCCTC TGCTGAATGC GCACGCAGCA ACCTCTGGGA 1440
 AACAGAGTAA CTTTTCCCGA AAATCATCCA CTCACAATAA GCCCTCTGAA GGCAAAGCGG 1500
 CAAACCCCAA AATGGTGAGC AGTCTCCCCA GCACCGCCGA CCCCTCTCAC CAGACCATGC 1560
 CGGCCAACAA GCAGAATGGA TCTTCTAACC AAAGACGGAG ATTTAATCCA CAGTATCATA 1620
 ACAACAGGCT AAATGGGCCT GCCAAGTCGC AGGGCAGTGG GAATGAAGCC GAGCCACTGG 1680
 GAAAGGGCAA CAGCCGCCAC GAACACAGAA GACAGCCGCA CAACGGCTTC CGGCCCAAAA 1740
 ACAAGGCGG TGCCAAAAT CAAGAGGCTT CCTTGGGGAT GAAGACCCC GAGGCCCCGG 1800

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CCCATTCTGA AAAGCCCCGG CGAAGGCAGC ACGCTGCAGA CACCTCGGAG GCCAGGCCCT 1860
TCCGGGGTAG TGTCGGTAGG GTTTCACAGT GCAATCTCTG CCCCACGAGA ATAGAAGTTT 1920
CCACAGATGC AGCAGTTCTC TCAGTCCCGG CTGTGACGTT GGTGGCCTGA GCTAGGAGGA 1980
AAAAGAGCAG TTTTCACTCA GTTTTGGTTC CCTGCCCAGG GTGCTGACCC AATTCGCTGC 2040
CAAAAGAGTG TCAATCAGAA TATACAAATC CCGTATGGTT GTGTCATCCT CTCTTAATCA 2100
TTTTTACTAA TTCTAATAAT CAGCTCTAGC TTGCTTCATA ATTTTCATGG CTTTGCTTGA 2160
TCTGTTGATG CTTTCTCTCA TCAAGACTTT GCAGCATTTT AGCCAGGCAG TATTTACTCA 2220
TTATTAGGAA AATCAAGATG TGGCTGAAGA TCAGAGGCTC AGTTAGCAAC CTGTGTTGTA 2280
GCAGTGATGT CAGTCCATTG ATTGTCTTTA GAGAGTTAAT GTTACAAAAA AGAATTCTTA 2340
ATAATCAGAC AAACATGATC TGCTGAGGAC ACATGCGCTT TTGTAGAATT TAACATCTGG 2400
TGTTTTTCTG AAAAAATATA TATACATATA TTGCTTTATT TGAAACAAAT TAAATATATGC 2460
TGCATTTGAA AAAAAAAA 2478

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1897 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: TESTTUT02
- (B) CLONE: 1273453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85 :

TGCACATCTA GCACAAATTG AAGATGATAG AGCTGCGATG GTTATTTCTT GGCATCTGGC 60
AAGTGACATG GACTGTGTAG TCACCCTAAC CACTGACGCT GCACGTCGTA TCTATGATGA 120
AACCCAAGGT CGTCAGCAGG TGTTGCCCCCT TGATTCTATT TACAAGAAGA CTCTTCCAGA 180
TTGGAAAAGA TCTCTACCTC ATTTCCGAAA TGGAAAATTG TATTTTAAAC CCATTGGAGA 240
TCCAGTCTTT GCTCGAGACT TGTTAACATT TCCAGATAAT GTAGAACATT GTGAAACAGT 300
ATTTGGTATG CTGTTAGGAG ACACCATTAT TTTGGATAAT CTGGATGCGG CCAATCATT 360
TAGAAAAGAG GTTGTAAAAA TTACACACTG TCCTACACTG CTGACCAGAG ATGGAGATCG 420
AATTCGAAGT AATGGAAAGT TTGGGGGCCT TCAGAATAAA GCTCCTCCAA TGGATAAACT 480
TCGGGGAATG GTATTTGGAG CTCCAGTTCC AAAACAGTGT CTGATCTTAG GGGAACAAAT 540
AGATCTTCTT CAGCAGTATC GTTCTGCTGT GTGCAAACTA GACAGTGTGA ATAAGGATCT 600

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TAACAGTCAA TTAGAGTACC TTCGCACTCC GGATATGAGG AAGAAAAAGC AAGAACTTGA 660
TGAACATGAG AAAAATCTCA AACTAATAGA GGAAAAACTA GGTATGACTC CCATACGTAA 720
GTGTAATGAC TCATTGCGTC ATTCACCAAA GGTGAGACG ACAGATTGTC CAGTTCCTCC 780
TAAAAGAATG AGACGAGAAG CTACAAGACA AAATAGGATT ATAACCAAAA CAGATGTATG 840
AGAGGTGACA GAGAGAAGAG GCCATTGGTC TCAGTAAGAA TGCCCTGCTT TCTGCATCTC 900
TGTTTCAGAA GACCAAGAGG GTGACTTACC AGACTGAGTA TTTCTGGGGA CAATACAAGT 960
ACCTGGGCAT GAATTTCCAT TTCGATTGAG ATGGGACTGG AAACAACCAT TCAATTTTAT 1020
GAATCTTACT GGACATTATG GATTTACTGG AATTATTCCA GACATTATGC CCTTTGGTTG 1080
TCACTACCTT GCAAATGTGT AAGAGGAAAA TGTGCTAATG TGGCAGTGAC TGTAAACTG 1140
GCACATGGCA TTTATTAATC CTGAAGAAAA GTACATGTAC TATTTTTCAG TATAAATATA 1200
ATGAACATGT CAGAACTATT TCTTGAAAAC CTTTTTATTA CTTTTCGCTG AATTTATTTA 1260
ACAAAGATGT TTTGTCTTTT GTGTAAGGGA GGTCTAGAG GCTAGATGTT TAATTGTAAA 1320
TATGTGAGGA AACTCAATGC AGAATTCAGG ATAAAAATTT TAAAAGCACA GGTATTTGGG 1380
AATTGAAATG TTAAGATACC CAGAACAACA TTAAATCAAT GAGTGAACCT GTGACAGTGG 1440
TAGCATTTCA AATTTCAAAA GACTTATCCT GTGTGTGTGT GTGTGTGTGT ATATATATAT 1500
ATATATATAT AAATATATAT ATATAAATA TTCAGCAGCA CCAAGTTTTA TAACTATTGT 1560
TTGTTTGAAT TTATTAATAC TAGAATATGT AGTCTCAGCC TTAATTTTAC ATTTACATTA 1620
TTTTGTAATT TTTTATTACT ATTTTAAAGG GGTTAAAGAG AACATACATT CTCACATTAG 1680
TGTAATTTCT GGTAGAAAGT TGCTGCAAAA ACATTTGAAA TGTATATTAA CCTAATGTAT 1740
GTCATATATA TGTCTTTGTG TAAGTTCAAG ACTATTGATC TGTGAAGTTA TTTTGTAAGG 1800
ACATACATTT GGTAAGTAAG TTTGTGTCCC AGGAAATGTA TGTGTTTTTA AACCCCTTCT 1860
AAATATGCAG GCCATTAATA AATAAGATTG TGTCTCA 1897

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1488 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: TESTTUT02
- (B) CLONE: 1275261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86 :

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CCCACGCGTC CGGGGACATC CTGTTCTGAG TCAAGATTCC TCCTTCTGAA CATGGGACTT 60
TCCAGAAGGA CCACAGCTCC TCCCGTGCAT CCACTCGGCC TGGGAGGTTT TGGATTTTGG 120
CTGTGCGAGGG AGTTTGCCTG CCTCTCCAGA GAAAGATGGT CATGAGGCCC CTGTGGAGTC 180
TGCTTCTCTG GGAAGCCCTA CTTCCCATTA CAGTTACTGG TGCCCAAGTG CTGAGCAAAG 240
TCGGGGGCTC GGTGCTGCTG GTGGCAGCGC GTCCCCCTGG CTTCCAAGTC CGTGAGGCTA 300
TCTGGCGATC TCTCTGGCCT TCAGAAGAGC TCCTGGCCAC GTTTTTCCGA GGCTCCCTGG 360
AGACTCTGTA CCATTCCCGC TTCCTGGGCC GAGCCCAGCT ACACAGCAAC CTCAGCCTGG 420
AGCTCGGGCC GCTGGAGTCT GGAGACAGCG GCAACTTCTC CGTGTGATG GTGGACACAA 480
GGGGCCAGCC CTGGACCCAG ACCCTCCAGC TCAAGGTGTA CGATGCAGTG CCCAGGCCCG 540
TGGTACAAGT GTTCATTGCT GTAGAAAGGG ATGCTCAGCC CTCCAAGACC TGCCAGGTTT 600
TCTTGTCTG TTGGGCCCCC AACATCAGCG AAATAACCTA TAGCTGGCGA CGGGAGACAA 660
CCATGGACTT TGGTATGGAA CCACACAGCC TCTTCACAGA CGGACAGGTG CTGAGCATTT 720
CCCTGGGACC AGGAGACAGA GATGTGGCCT ATTCTGCAT TGTCTCCAAC CCTGTCAGCT 780
GGGACTTGGC CACAGTCACG CCCTGGGATA GCTGTCATCA TGAGGCAGCA CCAGGGAAGG 840
CCTCCTACAA AGATGTGCTG CTGGTGGTGG TGCCTGTCTC GCTGCTCCTG ATGCTGGTTA 900
CTCTCTTCTC TGCCTGGCAC TGGTGCCCTT GCTCAGGGAA AAAGAAAAAG GATGTCCATG 960
CTGACAGAGT GGGTCCAGAG ACAGAGAACC CCCTTGTGCA GGATCTGCCA TAAAGGACAA 1020
TATGAACTGA TGCCTGGACT ATCAGTAACC CCACTGCACA GGCACACGAT GCTCTGGGAC 1080
ATAACTGGTG CCTGGAAATC ACCATGGTCC TCATATCTCC CATGGGAATC CTGTCCTGCC 1140
TCGAAGGAGC AGCCTGGGCA GCCATCACAC CACGAGGACA GGAAGCACCA GCACGTTTCA 1200
CACCTCCCCC TTCCCTCTCC CATCTTCTCA TATCCTGGCT CTTCTCTGGG CAAGATGAGC 1260
CAAGCAGAAC ATTCCATCCA GGACACTGGA AGTTCTCCAG GATCCAGATC CATGGGGACA 1320
TTAATAGTCC AAGGCATTCC CTCCCCACC ACTATTCTA AAGTACTAAC CAACTGGCAC 1380
CAAGAAAAAA TCCTCACTAA CCGCATCATC CGACAATAA TAATTCACAC TACATCCAAA 1440
CATCACTTAG GCGGCGGGGC CGCCGACTGG TTCCGGGCTT AGGGTGGG 1488

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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- (vii) IMMEDIATE SOURCE:
(A) LIBRARY: COLNNOT16
(B) CLONE: 1281682

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87 :

CCGACTTTGT AGCATTTTTA TTTAAGCTAA AACAGAGCAC ATGTATATGT ACATAAGACA 60
CATTAAATCT ATAAATACTA TTTATTTCATT TTATATAAAC TAATGTAATG GAAAACAAAT 120
TCTTATGACT TTGTGGTTTT ATAGATGTTT TAGAAACTTT GTATGTAGGT ATCTACAAAA 180
TTAGTTCATT CCCCTGAATA TTTTTCATT CATATTTTTG AGGTCTTGAT GTTTTCAGCC 240
TCTGGCGAAT CTTTTTCATT GAATTTGAAC CATTTGTAAA ATCTGTGATG CTGAAGCAGA 300
GTGTGTCACA AAGTGATGAG AACATTACTA AAATCCACGG ACGCACTGCG ACCTAAGGGC 360
TCAACGGCTG ACTCGGCAGC GGGCAGCCAC CCCACGCTCC CCTGCGGTCA CTCGCACACC 420
ACAGCCTGAA GCTCCCCCAG CGCCTGCACC TCGCACACAG CTAAGGTCAA AGTTCAAACG 480
CACTCCACAC GGAAGCTCAT TCTATACCCG AAGAGCAGTC TCAGAAAGCA AGATTACTTT 540
TGTGTTTTTT AAAAATGAT TCTTTAATGT ATTTTCTAA ACATTCTGAT TGGAAGTAGT 600
GGATTCCTAA ATGATTCCAA AGTCATCTGT AATTCTTCTG TTTTGTGTTT GTTCTGTCTT 660
TTCTTCATTT TGGCTTTGGG TGGGGGGAGG GGCAGGTGAC ACAAAGGATT TTTTTTTTTT 720
TTTTTTTTTA ATTTTGGAA TCTTTTCCAA TAACCAGCTA AAGATTGCA CTGAAATACA 780
ACTTGTATGC CTTTTGCATT TTTAAGCCT GCTTCCTGGA TTTAAGCAGA GTGATAGTGT 840
TCAAAGAGCC AGTTCAGCCT GTAACATATT TGAAAAAGAT ATGTCTGCAC TTTGAGGTCC 900
CTTTTGAATG CCATTCACTA GACCTCTCAA GCATTTTGTT TCATTGCTAC ATCCAAGCGC 960
CTCACAAGTC CACAATGCGG GACAGCATCA AAAGCTCAAG ACTTTGGAAA AAGCTTGTGG 1020
GCTTGCACTG GGGGAGGGAA GGGAACAAAA TTTGTGTACT TCTTTGTTTA ATTTAGAAAT 1080
AAGGCATCCA AGAGATGCCA TTATTTTCTG TGTTTCAATT GTTGTGCCTT TGAGTTAAAC 1140
TGCATTTTGT TCTTTTGTT GAAATCTGAA ATGTACTGTC CCAATATAAA ACAGTAATTA 1200
TTTGACCTTT GCACTGTTTG TCTGGTCCTT TTCAGTTTGA TTGCATATAA ATGTGGAAC 1260
TGATAGATCT CTATATTTTT AATGCACTTG TGATAAACTG GCAGCAGGGT TAGACATTAC 1320
TTTCAAAGCT TGAGGTAGAC CGAGTCAGCA TGCTAGA 1357

(2) INFORMATION FOR SEQ ID NO: 88:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2330 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: BRSTNOT07
(B) CLONE: 1298305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88 :

CCTACTTGTT CCCACCTTGG GAGAGGACGA TGA CT TGGGA GGGACGCGTG AAGGGAGAAG 60
GGGTCTCTCC ATGAGGCTGA GGATGGCCTG AACCTGGAGC AGCGGACCAG GCAGACGGGC 120
TGAAGTGGGG TCCCAAATTC CATGTCCAGA GGTGTGGGGA GCCTGCCTCC CTAGCTCCTG 180
GCCCCTGCCA GGGGCTTACA TCAAAACACC TCAGAGGGCT GCCCTCCAGA GGCTGCACCC 240
AGAACAGTGG GACATGAGCA GGGGTGTGGG CTTGGAGGGT GAAGAGGATG TGGTCCTATC 300
AGATGCTGGG CCTCCTCAGC CATAGCCCCC TGCTCCTACC CCCTGACTGG CTCTTGTTGTC 360
CTCACCTCTC ACCCTCTCCT TCCTGGGAGG CCCTGGGAGG TGATCATTGA CACCCAGCCA 420
AGCAGACAGC TGCGGGTGCC CAAGCCCTTG CTGGGCCTGC GCGTGAGGAG TCCCACTGCT 480
TCTAAAGGAA GTCCTGGGCA GGAGGTGGCT TTGGTGGTTG GTTCCAAAGT TGAAAATGCT 540
TGCAGTTTGA CCTTAGAAGA AGTGGGAAGA AGAAGGAGCT CTACAGGGTC AGCTTTGTTT 600
GATTTGTCCA GTCTAAGAAG TCCCAT TGCC AAAGCTTTCT GCAGGAGGGT GAATGCCGCA 660
GCTTGGCAGC CCCTGGGTTT CTCTTGAAA TGGTCAGTTT CCCCTCAAAG TACCCAAAGT 720
AGCCTTGCTG TGAGTTTTTG TCCTTGCTCT CTTTTTAGAG AAGAGGGCAT TTAGACTGCA 780
TTTTCTGCTG TAAAGAAGGT TAAAGCAAAT GTTTATTGCC TTTTCTAGTG AACTAACTCG 840
TAGAGATGTT CTCAGCAGGA AGACAGTCTT AGCACTGTCA CTTAGCAGAT TGCACTTAAG 900
TCCCTTGCTG TGGCCAGATG GCGTGGCTGG TTGCCTTAAT ATGTCCCAGG ACCCCTGACA 960
GGGCTGCCTG GCCTCTCCCT CGTGCTCCTC AAGAGCCCAG TCCATACACT GTGGATGTCA 1020
TTGCTGTCGG GTTAGGAAGT CTTGTCTTAG AACGCCCTGG CTGGTATGAC CACAGTTCAT 1080
GGCGGCTCTT CTCGCTTGGG TCATGGTCAT CTTCCAGCAC CTGCTGTGCT GGGGAAGGCCG 1140
AGGATGGGGG CCCAGCACTG TCCAGGCCTG CTGGGGCCTG GCTGGGAGTC CTGTGGGCAG 1200
CATGGAACAT GCAGCTGGGC TTCCTGTGAC CAGGCACCCT CTGGCACTGT TGCTTGCCCT 1260
GTGCCCTGGA CCTTTTCTG CCCTTCTCCT TCCTCTGCTC CCTTGGGGCT ACCCCTTGCC 1320
CCCTCCTGGT CTGTGCAAAC TCCCTCAGGG AGCCCCCTG CCCTGTAGCT CTCACTTAAC 1380
TTCCTAGGGG CTGCTGAGCC CACCCAGAGG TTGTTGGAGT TCAGCGGGGC AGCTTGCTCTC 1440
CCTTGTCAGC AGGGGCGTAA GGGCTGGGTT TGGCCATACA AGGTTGGCTA CGCCCTCAAT 1500
CCCTGACCGT TCCAGGCACT GAGCTGGGCA CCCACGGAAG GACATGCTGT CCAGACTGTG 1560

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ATGACTGCCA GCACAGGGCA TCTCGGGCTT GGCTGGTCTG CGAGGCCTTG CCCCTGTGGA 1620
ACTCTGGGTT CCTGTTTTCT CAGTCTTTTT GCGGCTTTGC TGTGGTTGGC AGCTGCCGTA 1680
CTCCAGGCTT GTGTCGGCCA CTCAGATGAG GGCTGTGGTG CGAGCCAGTG CAGGAGAGCT 1740
GCGCTTGGGA TTGTGCCCTC TCCTGTGTCT GTCCTCCGGA CCTACCCAGG TCTCCACCAT 1800
CAGGACCCTG TCTTTGGGTT TAGAAGACCA AGTATGGGGA AAACCAGACA CCAGCCTCTG 1860
CAGCAATGGG TCCCTCTAGC CTGTGGACAC CAGCTGGGGG ATCCAGGGTC AGGCCCCCTC 1920
CTCTCCCCAG TTTCCCTCTG CTGTGGGTTT TGGGCTGTCA TGTCTCCACC ACTTAAGGAT 1980
GTCTTTACAC TGAATTCAGG ATAGATGCTG GGATGCCTGG GCATGGCCAC ATGTTACATG 2040
TACAGAACTT TGTCTACAGC ACAAATTAAG TTATATAAAC ACAGTGAAGT GTATTTAATG 2100
CTGATCTACT ATAAGGTATT CTATATTTAT ATGACTTCAG AGACGCGTAT GTAATAAAGG 2160
ACGCCCTCCC TCCAGTGTCC ACATCCAGTT CACCCCAGAG GGTCGGGCAG GTTGACATAT 2220
TTATTTTTGT CTATTCTGTA GGCTTCCATG TCCAGAATCC TGCTTAAGGT TTTAGGGTAC 2280
CTTCAGTACT TTTTGCAATA AAAGTATTTT CTATCCAAAA AAAAAAAAAA 2330

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGNOT12
- (B) CLONE: 1360501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89 :

CTACACCTTT TCCATTTGCT AATAAGGCCC TGCCAGGCTG GGAGGGAATT GTCCCTGCCT 60
GCTTCTGGAG AAAGAAGATA TTGACACCAT CTACGGGCAC CATGGAAGT CTTCAAGTGA 120
CCATTCTTTT TCTTCTGCCC AGTATTTGCA GCAGTAACAG CACAGGTGTT TTAGAGGCAG 180
CTAATAATTC ACTTGTTGTT ACTACAACAA AACCATCTAT AACAACACCA AACACAGAAT 240
CATTACAGAA AAATGTTGTC ACACCAACAA CTGGAACAAC TCCTAAAGGA ACAATCACCA 300
ATGAATTACT TAAAATGTCT CTGATGTCAA CAGCTACTTT TTTAACAAGT AAAGATGAAG 360
GATTGAAAGC CACAACCACT GATGTCAGGA AGAATGACTC CATCATTTCA AACGTAACAG 420
TAACAAGTGT TACACTTCCA AATGCTGTTT CAACATTACA AAGTTCCAAA CCCAAGACTG 480
AAACTCAGAG TTCAATTAAA ACAACAGAAA TACCAGGTAG TGTTCTACAA CCAGATGCAT 540

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CACCTTCTAA AACTGGTACA TTAACCTCAA TACCAGTTAC AATTCCAGAA AACACCTCAC 600
AGTCTCAAGT AATAGGCACT GAGGGTGGAA AAAATGCAAG CACTTCAGCA ACCAGCCGGT 660
CTTATTCCAG TATTATTTTG CCGGTGGTTA TTGCTTTGAT TGTAATAACA CTTTCAGTAT 720
TTGTTCTGGT GGGTTTGTAC CGAATGTGCT GGAAGGCAGA TCCGGGCACA CCAGAAAATG 780
GAAATGATCA ACCTCAGTCT GATAAAGAGA GCGTGAAGCT TCTTACCGTT AAGACAATTT 840
CTCATGAGTC TGGTGAGCAC TCTGCACAAG GAAAAACCAA GAACTGACAG CTTGAGGAAT 900
TCTCTCCACA CCTAGGCAAT AATTACGCTT AATCTTCAGC TTCTATGCAC CAAGCGTGGA 960
AAAGGAGAAA GTCCTGCAGA ATCAATCCCG ACTTCCATAC CTGCTGCTGG ACTGTACCAG 1020
ACGTCTGTCC CAGTAAAGTG ATGTCCAGCT GACATGCAAT AATTTGATGG AATCAAAAAG 1080
AACCCCGGGG CTCTCCTGTT CTCTCACATT TAAAAATTCC ATTACTCCAT TTACAGGAGC 1140
GTTCTAGGA AAAGGAATTT TAGGAGGAGA ATTTGTGAGC AGTGAATCTG ACAGCCCAGG 1200
AGGTGGGCTC GCTGATAGGC ATGACTTTCC TTAATGTTTA AAGTTTTCCG GGCCAAGAAT 1260
TTTTATCCAT GAAGACTTTC CTACTTTTCT CCGTGTTCTT ATATTACCTA CTGTTAGTAT 1320
TTATTGTTTA CCACTATGTT AATGCAGGGA AAAGTTGCAC GTGTATTATT AAATATTAGG 1380
TAGAAATCAT ACCATGCTAC TTTGTACATA TAAGTATTTT ATTCCTGCTT TCGTGTTACT 1440
TTAATAAAT AACTACTGTA CTCAATACTC TAAAAATACT ATAACATGAC TGTGAAAATG 1500
GCAATGTTAT TGTCTTCCTA TAATTATGAA TATTTTTGGA TGGATTATTA GAATACATGA 1560
ACTCACTAAT GAAAGGCATT TGTAATAAGT CAGAAAGGGA CATAGGATTC ACATATCAGA 1620
CTGTTAGGGG GAGAGTAATT TATCAGTTCT TTGGTCTTTC TATTTGTCAT TCATACTATG 1680
TGATGAAGAT GTAAGTGCAA GGGCATTAT AACACTATAC TGCATTCAAT AAGATAATAG 1740
GATCATGATT TTTCATTAAC TCATTTGATT GATATTATCT CCATGCATTT TTTATTTCTT 1800
TTAGAAATGT AATTATTTGT TCTAGCAATC ATTGCTAACC TCTAGTTTGT AGAAAATCAA 1860
CACTTTATAA ATACATAATT ATGATATTAT TTTTCATTGT ATCACTGTTC TAAAAATACC 1920
ATATGATTAT AGCTGCCACT CCATCAGGAG CAAATTCTTC TGTTAAAAGC TAACTGATCA 1980
ACCTTGACCA CTTTTTTGAC ATGTGAGATC AAAGTGTCOA GTTGGCTGAG GTTTTTTGGG 2040
AAGCTTTAGA ACTAATAAGC TGCTGGTGGC AGCTTTGTAA CGTATGATTA TCTAAGCTGA 2100
TTTTGATGCT AAATTATCTT AGTGATCTAA GGGGCAGTTT AGTGAAGATG GAATCTTGTA 2160
TTTAAAATAG CCTTTTAAAA TTTGTTTTGT GGTGATGTAT TTTGACAACT TCCATCTTTA 2220
GGAGTTATAT AATCACCTTG ATTTTAGTTT CCTGATGTTT GGACTATTTA TAATCAAGGA 2280
CACCAAGCAA GCATAAGCAT ATCTATATTT CTGACTGGTG TCTCTTTGAG AAGGATGGGA 2340
AGTAGAAAAA AAAAAAAGAA AGAAAGGAAA GGAAGAGAGG AGAGAAGAAG GCAGGGATCT 2400

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CCACTATGTA TGTTCCTCACT TTAGAACTGT TGAGCCCATG CTTAATTTTA ATCTAGAAGT 2460
CTTTAAATGG TGAGACAGTG ACTGGAGCAT GCCAATCAGA GAGCATTGT CTTAGAAAA 2520
AAAAAAAATC TGAGTTTGGAG ACTAGCCTGG CCAACATGTT GAAACCCCAT ATCTACTAAA 2580
AATACAAAAA TTAGCCTGGT GTGGTGGCGC ACGCCTGTAG TCCCAGCTAC TCTGGAGCCT 2640
GAGGAACGTG AATCGCTTGA ACCCAGAAGA CAGAGGTTGC AGTGAGCTGA GATGGCACTA 2700
TTGCACTCCA GACTGGTGAC ACACGCAGA 2729

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGNOT12
- (B) CLONE: 1362406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90 :

GGCCCCGTGCA CTGCTCCTGA TCCCTGCTGC CCTCGCCTCT TTCATCCTGG CCTTTGGCAC 60
CGGAGTGGAG TTCGTGCGCT TTACCTCCCT TCGGCCACTT CTTGGAGGGA TCCCGGAGTC 120
TGGTGGTCCG GATGCCCCGCC AGGGATGGCT GGCTGCCCTG CAGACCGCAG CATCCTTGCC 180
CCCCTGGCAT GGGATCTGGG GCTCCTGCTT CTATTTGTTG GGCAGCACAG CCTCATGGCA 240
GCTGAAAGAG TGAAGGCATG GACATCCCGG TACTTTGGGG TCCTTCAGAG GTCAGTGTAT 300
GTGGCCTGCA CTGCCCTGGC CTTGCAGCTG GTGATGCGGT ACTGGGAGCC CATACCCAAA 360
GGCCCTGTGT TGTGGGAGGC TCGGGCTGAG CCATGGGCCA CCTGGGTGCC GCTCCTCTGC 420
TTTGTGCTCC ATGTCATCTC CTGGCTCCTC ATCTTTAGCA TCCTTCTCGT CTTTGAATAT 480
GCTGAGCTCA TGGGCCTCAA ACAGGTATAC TACCATGTGC TGGGGCTGGG CGAGCCTCTG 540
GCCCTGAAGT CTCCCCGGGC TCTCAGACTC TTCTCCACC TCGGCCACCC AGTGTGTGTG 600
GAGCTGCTGA CAGTGCTGTG GGTGGTGCTT ACCCTGGGCA CGGACCGTCT CCTCCTTGCT 660
TTCTCCTTA CCCTCTACCT GGGCCTGGCT CACGGGCTTG ATCAGCAAGA CCTCCGCTAC 720
CTCCGGGCCC AGCTACAAAG AAAACTCCAC CTGCTCTCTC GGCCCCAGGA TGGGGAGGCA 780
GAGTGAGGAG CTCAGTCTGG TTACAAGCCC TGTCTTCTCT CTCCCACTGA ATTCTAAATC 840
CTTAACATCC AGGCCCTGGC TGCTTCATGC CAGAGGCCCA AATCCATGGA CTGAAGGAGA 900
TGCCCTTCT ACTACTTGAG ACTTTATTCT CTGGGTCCAG CTCCATACCC TAAATTCTGA 960

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GTTTCAGCCA CTGAACTCCA AGGTCCACTT CTCACCAGCA AGGAAGAGTG GGGTATGGAA 1020
GTCATCTGTC CCTTCACTGT TTAGAGCATG AACTCTCCC CCTCAACAGC CTCCTGAGAA 1080
GGAAAGGATC TGCCCTGACC ACTCCCCTGG CACTGTTACT TGCCTCTGCG CCTCAGGGGT 1140
CCCCTTCTGC ACCGCTGGCT TCCACTCCAA GAAGGTGGAC CAGGGTCTGC AAGTTCAACG 1200
GTCATAGCTG TCCCTCCAGG CCCCAACCTT GCCTCACCAC TCCCGGCCCT AGTCTCTGCA 1260
CCTCCTTAGG CCCTGCCTCT GGGCTCAGAC CCCAACCTAG TCAAGGGGAT TCTCCTGCTC 1320
TTAACTCGAT GACTTGGGGC TCCCTGCTCT CCCGAGGAAG ATGCTCTGCA GGAAAATAAA 1380
AGTCAG 1386

(2) INFORMATION FOR SEQ ID NO: 91:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 542 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
(A) LIBRARY: LATRTUT02
(B) CLONE: 1405329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91 :

CCCGGGCCAT GCAGCCTCGG CCCCGCGGGC GCGCGCCGCG CACCCGAGGA GATGAGGCTC 60
CGCAATGGCA CCTTCTGAC GCTGCTGCTC TTCTGCCTGT GCGCCTTCCT CTCGCTGTCC 120
TGGTACGCGG CACTCAGCGG CCAGAAAGGC GACGTTGTGG ACGTTTACCA GCGGGAGTTC 180
CTGGCGCTGC GCGATCGGTT GCACGCAGCT GAGCAGGAGA GCCTCAAGCG CTCCAAGGAG 240
CTCAACCTGG TGCTGGACGA GATCAAGAGG GCCGTGTCAG AAAGGCAGGC GCTGCGAGAC 300
GGAGACGGCA ATCGCACCTG GGGCCGCCTA ACAGAGGACC CCCGATTGAC GCCGTGGAAC 360
GGCTCACACC GGCACGTGCT GCACCTGCCC ACCGTCTTCC ATCACCTGCC ACACCTGCTG 420
GCCAAGGAGA GCAGTCTGCA GCGCGCGGTG CGCGTGGGCC AGGGCCGCAC CGGAGTGTCTG 480
GTGGTGATGG GCATCCCGAG CGTGCGGCGC GAGGTGCACT CGTACCTGAC TGACACTCTG 540
CA 542

(2) INFORMATION FOR SEQ ID NO: 92:

- (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 772 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAINOT12
- (B) CLONE: 1415223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92 :

CGAGCCCGGA GTGCGGACAC CCCCGGGATG CTTGCGCCCC AGAGGACCCG CGCCCCAAGC 60
CCCCGCGCCG CCCCCAGGCC CACCCGGAGC ATGCTGCCTG CAGCCATGAA GGGCCTCGGC 120
CTGGCGCTGC TGGCCGTCCT GCTGTGCTCG GCGCCCGCTC ATGGCCTGTG GTGCCAGGAC 180
TGCACCCTGA CCACCAACTC CAGCCATTGC ACCCAAAGC AGTGCCAGCC GTCCGACACG 240
GTGTGTGCCA GTGTCCGAAT CACCGATCCC AGCAGCAGCA GGAAGGATCA CTCGGTGAAC 300
AAGATGTGTG CCTCCTCCTG TGACTTCGTT AAGCGACACT TTTTCTCAGA CTATCTGATG 360
GGGTTTATTA ACTCTGGGAT CTTAAAGGTC GACGTGGACT GCTGCGAGAA GGATTTGTGC 420
AATGGGGCGG CAGGGGCAGG GCACAGCCCC TGGGCCCTGG CCGGGGGGCT CCTGCTCAGC 480
CTGGGGCCTG CCCTCCTCTG GGCTGGGCCC TGATGTCTCC TGCTTCCCAC GGGGCTTCTG 540
AGCTTGCTCC CCTGAGCCTG TGGCTGCCCT CTCCCAGCC TGGCGTGGCT GGGGCTGGGG 600
GCAGCCTTGG GCCAGCTCCG TGGCTGTGGC CTGTGGGTCT GAATTCTTCC CCGACGTGAA 660
GCCTNCCTGT CTCTCCGGCA GCTCTGAGTC CCAGGCAGCT GGACATTCCA GGGGAACAAG 720
CCATTNGGCA GGAGGGCTGG GATGAGGTTG GGGGGGACCG GAGGTCCCGG AG 772

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1738 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAINOT12
- (B) CLONE: 1416553

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93 :

TGTCCATCCA AAAACCATAA AATCACTGGG TTCCACATCA GCCTCCATGA GGCCAAGCCT 60
TGTACCTGCA AGCTCTTGGC CTAACCATTC CTCTGTCTC TTCTCTGGCC TGCCTGGGGA 120
GCCCCGTGAAG GCCGCACGGG TGCCTCCAGC CTGAGACATC AGGGGAGAGC CTGCAGCTGA 180

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GTTCAGCAGA AAGGAGGAAT CCTGGCCCTC AGGAAGAAGA TAGTCACATG TTTTCTTCC 240
TTGTCCCCAC AGCCCCCAGA ACAACATTCT CCCTGCTGGC AGCCCTTCCA TGTCTCCAAA 300
CCTGGGTCAG AGTGAAAGGA CCTTTGGGGG TGGGTGGGAG CAAAGGGCCC ACCTGCTGGT 360
TGGTGAAAGC AGTGGTGCCG GAGTGCTAGG TACCGCACGA GTAGTGGTGC GGGGGCTTGG 420
GAAGCAGACC AGGGTTGGAC AAAACCCCAT GAGGGCGGGG AGCTGGAAGA AAAGTCTCTT 480
GGGGACCTCT GGGGCAAGGA GCTGAGAAGT CCTGCAGCAC CAGGTGAGAC TTGCTTACAG 540
TGGATGCCAC TTCTAGGCCT CTGGACCGCA GATGCCCTCC TCCCTCCTGC ACACCTGGCC 600
TCCTGGGCCT CCAGGTAAAG AGAGAGAGCC AGCCCAGCCC TGTTTCCCCT CAGTCCTCCT 660
TTGCTCCTGC TGCTTCTCCC AACAGCCCAC TGTTAGGAGG TAGTAGACCC CAGCCTCAAG 720
GCTCTGACCT TCTTCATGTG GGCACAGAGG GTCCTGACAC TCTGGCAGGG CCTGAGCTGG 780
GGCAGGCCTC CCTCAGGGCC AGGGGCGATG GCACCCCGGG GACAGGCAGA CCTCCTTCCT 840
GCCGTCAGCA CCCCCTTCCT TATCACTGTC TGGTCTCCGA GCTTCGGCTG CAGCCTGAGG 900
TGTGTCCTGG GCTCCTCAGA GCCTGAAGCA AGCTTTTGGA AGCCTGCAGT CCTCCCAGCT 960
CCAGTGCAGA AGCCTCTCTC TCCAGCCTTT CCCCAGGCAG GAGTTGGGGT TGGGGGCCTC 1020
TGTCCTCAT CGCTTACCTT GGAAAGGTGG GAAGCTGGCA ATCTGCACCT TGGGGCCTGG 1080
GCTCCCCCTC TCTGTGCCAG CGGCTTCCCA GCACCTGGGA GGGGCTGCAG CCCCAGCTGG 1140
ACTCCAGCCT GTCCCTCTTA GCACTCTAGC TGCCCACTCC AGGGCAGGGA CTCGAAACCC 1200
CCTCCGTCCT GAGCAGCCAC CTCCAGGGCC CTGTTTGGA CCACTCTCTC AGTCCCCAGG 1260
TCCTCAGGGC CCCAGAGCGG GAGGGTCTCC TACCTGGAAG TCCCCCTGAG CTCCAGGGCC 1320
CAGCCCTACC TGCCAGTGCT GGTGTCAGGG CACTCAACAC CGAGTGTGGG GGCCACGCCC 1380
CTTGCCATGC CCACGGCCTC CTCCTGTAGC CCCTGCCTGC ACCCACGATG CTGCACGGGC 1440
CCGCCCTGGT GGGGCTCGGC GAGTAATGTG TTTTGTCCCC AGTTAACCAC CATTCTGCGG 1500
CCTGGTTCTG CAAGGAACCA GGGCTGCCCC ACCGCCCGCC GTCTGCCGCC CTAGGCTTCC 1560
TGA CTCCATT AGTTCCGACA CTTGTGAAAC TCCGAGAAGT GCTGTGGTCT CAGCAATGCA 1620
CCTGTTTTGT ACATGATTGT GTAATTTAAA GGTATATAAA TACAAATATA TATATATATC 1680
AGTTGTGATT GTATGACTGT GGATAAAATC CAGAACTGTG TCAACCTGAA AAAAAAAA 1738

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2100 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: KIDNNOT09
(B) CLONE: 1418517

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94 :

GGGAAAGCGG CGAGTAAGAT GGAAGATGAG GAGGTCGCTG AGAGCTGGGA AGAGGCGGCA 60
GACAGCGGGG AAATAGACAG ACGGTTGGAA AAAAAACTGA AGATCACACA AAAAGAGAGC 120
AGGAAATCCA AATCTCCTCC CAAAGTGCCC ATTGTGATTC AGGACGATAG CCTTCCCGCG 180
GGGCCCCCTC CACAGATCCG CATCCTCAAG AGGCCCACCA GCAACGGTGT GGTCAGCAGC 240
CCCAACTCCA CCAGCAGGCC CACCCTTCCA GTCAAGTCCC TAGCACAGCG AGAGGCCGAG 300
TACGCCGAGG CCCGGAAGCG GATCCTGGGC AGCGCCAGCC CCGAGGAGGA GCAGGAGAAA 360
CCCATCCTCG ACAGGCCAAC CAGGATCTCC CAACCCGAAG ACAGCAGGCA GCCCAATAAT 420
GTGATCAGAC AGCCTTTGGG TCCTGATGGG TCTCAAGGCT TCAAACAGCG CAGATAAATG 480
CAGGCAAGAA AAGATGCCGC CGTTGCTGCC GTCACCGCCT CCTGGGTCGT CCGCCACGGG 540
TTGCACTGCC GTGGCAGACA GCTGGACTTG AGCAGAGGGA ACGACCTGAC TTACTTGAC 600
TGTGATCCCC CTTGCTCCGC CCACTGTGAC CTTGAACCCC ATGCACTGTG ACCTCCCCCC 660
TTCTCCCCCT TCCCACTGTG ATTGGCACAT CGACAAGGGC TGTCCCAAGT CAATGGAAAG 720
GGAAAGGGTG GGGGTTAGGG GAAGGTTGGG GGGACCCAGC AAGGACTCAG AGAGTCAGAC 780
AGTGCCACTT GGCCACTTGG GGTAAAGCCA GTGCCAGCAA TAACAGTTTA TCATGCTCAT 840
TAATTTGGGA TTTCAAACA CAAATGAAAA CTCACACCCA CCCACCCCA AGTGCATGTC 900
TCCATCACTT AAAAAGTAAG TTCCATTTGA AAATATCCTT TCTTTTTTTT TTCTTCTAT 960
TTTTGTTTGT TTATACAAAT ATCTGATTTG CAAGAAAAAG TGCATGGGAG GGGTTTTAGT 1020
GGTTTAATGA ATTTTAAATT AAGAAAGGGT AGTTTGGTAG TCTACTTAAA AATGTTTCTG 1080
GGAAATTCAC TAGAAACATT AACCAATAGG ATTTTGGTGA GCTTAGCTTC TGTATTCTTA 1140
CTGCCGCCCA GAAAAGGGGC AGGGCTCTGC AGCCGCCAGG ACAGACGAGC ACCCATGCC 1200
TATACCTCCC TCCCCGAGCT AAGTCCCAGG GCATCTGGGC CTTGCCTGGA GACTGGGCTA 1260
GCTCTGTAGG CTCGGAGAGC CTGGGGAGGG TGCCAACCCC ACCTCTAGTA TTTTGGGAGA 1320
TAGGGAAAGT GAACCGACTT CCCCTTCCCA TACCCCTCAG GGTGGTTCCC TACCAGCCAG 1380
GCTTACTACT TCTAGAAGAA AGCAGAGTGC CAGGGAGTGA GATTGCATCC CTGGGCTTAG 1440
AAGTGACGGA GAGAAGACTT GTTTAGTATT TTGCCATCAG CACAAGGAAA ACCAGGAGAG 1500
AGTCTGCCTC CAGGACTCTG AGCCTTCTGC CTCGTATGTT CAGAAGGTGG ATAGGTCTTC 1560

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CCACTCCAGC ATGGCTTGAA CTCTTAGGGG TCTGCAGTGC TCCATCTCCA TTGGTGGCCC 1620
CAGCTCAGTA ACTATACCTG GTACATTTCC TGTGTGCAAT CAGTACCTTG AAGGCAGAAC 1680
ATTCTGAATA AAGTTGGAAG AAGAACAGCT TTGCTTTGCA AAGATTGATG ACAGACTGGT 1740
TCCTCAGAGG CCTAGGCTAC CCGTCACCCC TTTTTCAGAG GCGAGGGCCT GGAATGAAGG 1800
CAGTTTATCC TCTGTCCCTG GAGCCTGGGG TTTGCTTTGG CTCCTTGAGG TGGAAGAGAC 1860
TAAGAGGGCA GCTGCCCAGA GCAGCTGTGT GTACCTGGCT CCTCTCAGGC TTCCTGATCC 1920
CTTCCATTGC ACTGCGCCTT ATCCCTCAGC CAGCCAGACA GCCTCCCTGC TCCTGACCAG 1980
CAGATACGTT TCGGAGTGGT TGGTGTGGTT TTTGTGATGA GGGCAGCACA TGGTGGCCAA 2040
GGTGGGCAAA GCTGAGTCTC ACAAGGCTCA AATCCCTTCG GTTGGGNTCC CCTTGTGGGG 2100

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PANCNOT08
- (B) CLONE: 1438165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95 :

GCGGGCGGAG ATGTAGACCC GGTAGTGTTG TGCCTTGTGG TGACAACTGG CGGCAGCGCG 60
CCGCGGGCCC GAGACTTAGT CTCGGGCCGC CATGGCCAGC GTCCACGAGA GCCTCTACTT 120
CAATCCCATG ATGACCAATG GGGTTGTGCA CGCCAATGTG TTCGGCATCA AGGACTGGGT 180
GACGCCGTAC AAGATCGCGG TGCTGGTGCT GCTGAACGAG ATGAGCCGCA CAGGCGAGGG 240
CGCCGTCAGC CTCATGGAGC GGCGGAGGCT CAACCAGCTG CTCCTGCCCC TGCTGCAGGG 300
CCCAGATATT AACTGTCAA AACTTTACAA GTTAATTGAA GAGTCTTGTC CACAGCTGGC 360
AAATTCAGTG CAGATCAGAA TCAAACATGAT GGCTGAAGGC GAGTTGAAGG ATATGGAACA 420
GTTTTTTGAT GACCTTTCAG ATTCTTTCTC TGGAACAGAA CCAGAGGTTT ACAAACAAG 480
TGTAGTAGGT TTGTTTCTGC GTCACATGAT CTTGGCCTAC AGTAAGCTTT CTTTCAGCCA 540
AGTGTTTAAA CTGTACACTG CCCTTCAGCA GTACTTCCAG AATGGTGAGA AAAAGACAGT 600
GGAGGATGCT GATATGGAAC TGACCAGTAG AGATGAGGGT GAAAGAAAAA TGGAAGAAAG 660
AGAACTTGAT GTATCTGTAA GAGAAGAGGA GGTATCTTGC AGTGGGCCTC TGTCCCAAAA 720
ACAAGCAGAA TTTTTTCTTT CTCAACAGGC TTCTTTGCTA AAGAATGATG AGACTAAGGC 780

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CCTCACTCCA GCTTCCTTGC AGAAGGAATT AAACAATTTG TTGAAATTTA ATCCTGATTT 840
TGCTGAAGCG CATTATCTCA GCTACTTAAA CAACCTCCGT GTCCAAGATG TTTTCAGTTC 900
AACACACAGT CTCCTCCATT ATTTTGATCG TCTGATTCTT ACCGGAGCCG AAAGCAAAAG 960
TAATGGGGAA GAGGGCTATG GCCGGAGCTT GAGATACGCC GCTCTGAATC TTGCCGCCCT 1020
GCACTGCCGC TTCGGTCACT ATCAACAGGC AGAGCTCGCC CTGCAGGAGG CAATTAGGAT 1080
TGCCCAGGAG TCCAACGATC ACGTGTGTCT CCAGCACTGT TTGAGCTGGC TTTATGTGCT 1140
GGGGCAGAAG AGATCCGATA GCTATGTTCT GCTGGAGCAT TCTGTGAAGA AGGCAGTACA 1200
TTTTGGGTTA CCGAGAGCTT TTGCTGGGAA GACGGCAAAC AAGCTGATGG ATGCCCTAAA 1260
GGACTCCGAC CTCCTGCACT GGAAACACAG CCTGTCAGAG CTCATCGATA TCAGCATCGC 1320
ACAGAAAACG GCCATCTGGA GGCTGTATGG CCGCAGCACC ATGGCACTGC AACAGGCCCA 1380
GATGTTGCTG AGCATGAACA GCCTGGAGGC GGTGAATGCG GGCGTGCAGC AGAACAACAC 1440
AGAGTCCTTT GCTGTGCAC TCTGCCACCT CGCAGAGCTA CACGCGGAGC AGGGCTGTTT 1500
TGCTGCAGCT TCTGAAGTGT TAAAGCACTT GAAGGAACGA TTTCCGCTA ATAGTCAGCA 1560
CGCCCAGTTA TGGATGCTAT GTGATCAAAA AATACAGTTT GACAGAGCAA TGAATGATGG 1620
CAAATATCAT TTGGCTGATT CACTTGTTAC AGGAATCACA GCTCTCAATA GCATAGAGGG 1680
TGTTTATAGG AAAGCGGTTG TATTACAAGC TCAGAACCAA ATGTCAGAGG CACATAAGCT 1740
TTTACAAAAA TTGTTGGTTC ATTGTCAGAA ACTGAAGAAC ACAGAAATGG TGATCAGTGT 1800
CCTACTGTCC GTGGCAGAGC TGTACTGGCG ATCTTCCTCC CCTACCATCG CGCTGCCCAT 1860
GCTCCTGCAG GCTCTGGCCC TCTCCAAGGA GTACCGGTTA CAGTACTTGG CCTCTGAAAC 1920
AGTGCTGAAC TTGGCTTTTG CGCAGCTCAT TCTTGAATC CCAGAACAGG CCTTAAGTCT 1980
TCTCCACATG GCCATCGAGC CCATCTTGGC TGACGGGGCT ATCCTGGACA AAGGTCGTGC 2040
CATGTTCTTA GTGGCCAAGT GCCAGGTGGC TTCAGCAGCT TCCTACGATC AGCCGAAGAA 2100
AGCAGAAGCT CTGGAGGCTG CCATCGAGAA CCTCAATGAA GCCAAGAAGT ATTTTGCAAA 2160
GGTTGACTGC AAAGAGCGCA TCAGGGACGT CGTTTACTTC CAGGCCAGAC TCTACCATAC 2220
CCTGGGGAAG ACCCAGGAGA GGAACCGGTG TGCGATGCTC TTCCGGCAGC TGCATCAGGA 2280
GCTGCCCTCT CATGGGGTAC CCTTGATAAA CCATCTCTAG AGAGGACATC CCTGCTGGGC 2340
TGCTGTGCAG AGTATAAGAT TTTGGACTTG TTCATGTCCC CTCTCTCCCT ATAAATGATG 2400
TATTTGTGAC ACCCTATCTT GTCAATAAAC AGCATTCTGA TTAAAAAAA AAAAAAAA 2458

(2) INFORMATION FOR SEQ ID NO: 96:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2900 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
 (A) LIBRARY: THYRNOT03
 (B) CLONE: 1440381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96 :

TGCATGGATG GGATACTGGA TGAATCTTTG CTTGAAACCT GTCCAATTCA GTCACCATTA 60
 CAAGTTTTTG CAGGAATGGG TGGACTGGCT CTTATTGCTG AAAGACTACC CATGCTATAT 120
 CCAGAAAGTAA TTCAACAGGT GAGTGCTCCA GTTGTAACAT CTACCACTCA GGAAAAGCCG 180
 TATGATAGCG ATCAGTTTGA ATGGGTGACC ATTGAACAGT CAGGGGAGTT AGTTTATGAA 240
 GCACCAGAAA CTGTTGCGGC TGAACCTCCA CCTATCAAGT CAGCAGTACA GACCATGTCT 300
 CCCATACCTG CCCATTCTTT GGCTGCTTTT GGATTATTTT TTCGTCTTCC GGGCTATGCG 360
 GAAGTGCTAC TGAAAGAGAG AAAACATGCC CAGTGCCTTC TTCGATTGGT ATTGGGAGTG 420
 ACAGATGATG GAGAAGGAAG TCATATTCTT CAATCTCCAT CAGCCAATGT GCTTCCAACC 480
 CTTCTTTTCC ACGTCCTTCG TAGCTTGTTT AGCACTACAC CTTTGACAAC TGATGATGGT 540
 GTACTTCTAA GGCGGATGGC ATTGGAAATT GGAGCCTTAC ACCTCATTCT TGTCTGTCTC 600
 TCTGCTTTGA GCCACCATTG CCCACGAGTT CCAAACCTCTA GCGTGAATCA AACTGAGCCA 660
 CAGGTGTCAA GCTCTCATAA CCCTACATCA ACAGAAGAAC AACAGTTATA TTGGGCCAAA 720
 GGGACTGGCT TTGGAACAGG CTCTACAGCT TCTGGGTGGG ATGTGGAACA AGCCTTAACT 780
 AAGCAAAGGC TGGAAGAGGA ACATGTTACC TGCCTTCTGC AGGTTCTTGC CAGTTACATA 840
 AATCCCGTCA GTAGTGCGGT AAATGGAGAA GCTCAGTCAT CTCATGAGAC TAGAGGGCAG 900
 AACAGTAATG CCCTTCCTTC TGTACTTCTC GAGCTTCTCA GTCAGTCCTG CCTCATCCCA 960
 GCCATGTCAT CTTATCTACG AAATGATTCA GTTCTGGACA TGGCAAGACA TGTGCCACTC 1020
 TATCGGGCAC TGCTGGAATT GCTTCGGGCC ATTGCTTCTT GTGCTGCCAT GGTGCCCCCTA 1080
 TTGTTGCCCC TTTCTACAGA GAACGGTGAA GAGGAAGAAG AACAGTCAGA ATGTCAAACCT 1140
 TCTGTTGGTA CATTGTTAGC CAAAATGAAG ACCTGTGTTG ATACCTATAC CAACCGTTTA 1200
 AGATCTAAAA GGGAAAATGT TAAAACAGGA GTAAAACCAG ATGCGTCTGA TCAAGAACCA 1260
 GAAGGACTTA CTCTTTTGGT ACCAGACATC CAAAAGACTG CTGAGATAGT TTATGCAGCC 1320
 ACCACCAGTT TGCGGCAAGC AAATCAGGAA AAAAAGCTGGG TGAATACTCC AAGAAGGCGG 1380
 CTAATGAACC CCAAACCTTT GTCAGTATTA AAGTCACTTG AAGAAAAATA TGTGGCTGTT 1440
 ATGAAGAAAT TACAGTTTGA TACGTTTGAA ATGGTTTCTG AAGATGAAGA TGGGAAATTG 1500

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GGATTTAAAG TAAATTACCA CTACATGTCT CAGGTGAAAA ATGCTAATGA TGCGAACAGT 1560
GCTGCCAGAG CTCGCCGCCT TGCCCAGGAA GCTGTGACGC TTTCAACCTC ACTGCCTCTG 1620
TCTTCATCCT CTAGTGTGTT TGTACGCTGT GATGAGGAGC GACTTGATAT CATGAAGGTT 1680
CTAATAACTG GTCCAGCGGA CACCCCTTAT GCAAATGGCT GCTTTGAGTT TGATGTGTAT 1740
TTTCCTCAAG ATTATCCCAG TTCACCCCTT CTTGTGAATC TAGAGACAAC TGGTGGTCAT 1800
AGCGTGCGAT TCAATCCAAA CCTTTATAAT GATGGCAAGG TTTGTTTAAG CATCTTAAAC 1860
ACGTGGCATG GAAGACCAGA AGAGAAGTGG AATCCTCAGA CCTCAAGCTT TTTGCAAGTG 1920
TTGGTGTCTG TCCAGTCCCT TATATTAGTA GCTGAGCCTT ATTTTAATGA ACCGGGATAT 1980
GAACGGTCTA GAGGCACTCC CAGTGGCACA CAGAGTTCTC GAGAATATGA TGGAAACATT 2040
CGACAAGCAA CAGTTAAGTG GGCAATGCTA GAACAAATCA GAAACCCTTC ACCATGTTTT 2100
AAAGAGGTAA TACACAAACA TTTTACTTG AAAAGAGTTG AGATAATGGC CCAATGTGAG 2160
GAGTGGATTG CGGATATCCA GCAGTACAGC AGTGATAAGC GGGTAGGCAG GACTATGTCT 2220
CACCATGCAG CAGCTCTCAA GCGTCACACT GCTCAGCTCC GCGAAGAGTT GCTGAAACTT 2280
CCCTGCCCTG AAGGCTTGGA TCCTGACACT GACGATGCC CAGAGGTGTG CAGAGCCACA 2340
ACAGGTGCTG AGGAGACTCT AATGCATGAT CAGGTTAAAC CCAGCAGCAG CAAAGAACTC 2400
CCCAGTGACT TCCAGTTATG AGCTGCATTG ATGTGGACTT CATAGACACA AAGGCTTCGA 2460
AGCACAAGCC AAATATGTCA ATATTTGTAT GTAAGAACT AATTATGTAA TAGGTAATGA 2520
AACTGAACT ATACTATGCC CTTAAGGAGA TCCAGTTTAA TTCAAGGTGA TCTTTTATTT 2580
ACCTGTACAG GAGTGTAAC TTTTTTGTGC TTTTATTTTT CAATTGTGAG AACCCTGAT 2640
TGGTATGTTT AACAAATTTG TGTATACAAA GAAATGGATA AATCACTGCT ATATAAGGGA 2700
AACTACCTTA GGAAAGAATG TTTACTGAAT GTTTATTTTA TTTTATTTTT TTTTACTAT 2760
AGAGTGAGGG GTTGTTAACA AAGAATATAT ATTGGTCGTT CTTACAATA CTATTTAAAG 2820
TCAGCAACTT TTTACTGAAT TTGATAGATT TTATGTTTGG GGGTACGAGC TTGTAAAGCT 2880
CGGGTGCCTN ATGAGTGACC 2900

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

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(A) LIBRARY: LUNGNOT14

(B) CLONE: 1510839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97 :

CCGCTGAGAT GTACGAACTT CCGGTTCTCC GGGCAGCTGC CACTGCTGTA GCTTCTGCCA 60
CCTGCCACGA CCGGGCCTCT CCCTGGCGTT TGGTCACCTC TGCTTCATTC TCCACCGCGC 120
CTATGGTCCC TCTTGAGACC AGCGTGGCGG GCCTGGCGGC TCCCGGGTGG TGAGAGAGCG 180
GTCCGGGAAC GATGAAGGCC TCGCAGTGCT GCTGCTGTCT CAGCCACCTC TTGGCTTCCG 240
TCCTCCTCCT GCTGTTGCTG CCTGAACTAA GCGGGCCCCCT GGCAGTCCTG CTGCAGGCAG 300
CCGAGGCCGC GCCAGGTCTT GGGCCTCCTG ACCCTAGACC ACGGACATTA CCGCCGCTGC 360
CACCGGGCCC TACCCCTGCC CAGCAGCCGG GCCGTGGTCT GGCTGAAGCT GCGGGGCCGC 420
GGGGCTCCGA GGGAGGCAAT GGCAGCAACC CTGTGGCCGG GCTTGAGACG GACGATCACG 480
GAGGGAAGGC CGGGGAAGGC TCGGTGGGTG GCGGCCCTTG TGTGAGCCCC AACCTGGCG 540
ACAAGCCCAT GACCCAGCGG GCCCTGACCG TGTGATGGT GGTGAGCGGC GCGGTGCTGG 600
TGTACTIONCGT GGTGAGGACG GTCAGGATGA GAAGAAGAAA CCGAAAGACT AGGAGATATG 660
GAGTTTTTGA CACTAACATA GAAAATATGG AATTGACACC TTTAGAACAG GATGATGAGG 720
ATGATGACAA CACGTTGTTT GATGCCAATC ATCCTCGAAG AAGAGAATGT GCCTTTTGAT 780
GAAAGAACTT TATCTTTCTA CAATGAAGAG TGGAATTTCT ATGTTTAAGG AATAAGAAGC 840
CACTATATCA ATGTTGGGGG GGTATTTAAG TTACATATAT TTTAACAACC TTTAATTTGC 900
TGTTGCAATA AATACCGTAT CCTTTTATTA TATCTTTATA TGTATAGAAG TACTCTATTA 960
ATGGGCTCAG AGATGTTGGG GATAAAGTAT ACTGTAATAA TTTATCTGTT TGAAAATTAC 1020
TATAAAACGG TGTTTTCTGA TCGGTTTTTG TTTCTGCTT ACCATATGAT TGTAATTGT 1080
TTTATGTATT AATCAGTTAA TGCTAATTAT TTTTGCTGAT GTCATATGTT AAAGAGCTAT 1140
AAATTCCAAC AACCAACTGG TGTGTAAAAA TAATTTAAAA TTTCTTTTAC TGAAAGGTAT 1200
TTCCCATTTT TGTGGGGAAA AGAAGCCAAA TTTATTACTT TGTGTTGGGG TTTTAAAAAT 1260
ATTAAGAAAT GTCTAAGTTA TTGTTTGCAA AACAATAAAT ATGATTTTAG 1310

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2272 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

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(vii) IMMEDIATE SOURCE:
(A) LIBRARY: SPLNNOT04
(B) CLONE: 1534876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98 :

CCATGCTCCA GGCATACAGA TGTGGTTTCT CGGCTGCACC GGGCCAGGCT GCGGGTGTGC 60
AGGCGTCTGC AAAGTTGTGC CATGTATCAG CACAGGCTTT GAGACGTCTG GACCCTGTCC 120
TTCTCCCCGT GAGGGGTTCT TGTTCTTTCT GACTCAGGTG ACTTTTCAGC CCTTCCAATT 180
CCCCTCTTTT TCTGCCCTCC CCTCCAACCTC AGCCAACCCA GGTGTGGGCA GTCAGGGAGG 240
GAGGGAGTGT CCCACCACGT TCTCAGGGCA GCCCTTGACT CCTAAGCCCC TTCCTCCTTC 300
CATTTCTGCAT CCCCTCCCCA TCCAACCTAA ATGCCACAG CTGGGGCTGA GCTGTATTCC 360
TGTGGAGGGA CCTCTGCCGT GCCTCTCTGA GGTCAGGCTG TGCTGTGTGA TGGGCAGGCT 420
TTGCCCCAGC CCACCCCTGG CAAGGTGCAC TTGTTTTCTG GTTTGTACAA GGTGTCTCTG 480
GGGCCCCGTCG CTTCCCTGCC AGTGAGGAGT GACTTCTCCC TCTCTTCCAG TCCTGTAGGG 540
GAGACAAAAC CAGATTGGGG GGCCCAAGGG GAGCATGGAA AAGGCCGGCT CCCCTGTCTT 600
TCCTTGGCTG TCAGAGTCAG GGTAACACAC ACCAAGAGTG GAGTGCGGCC AGCAAGTTTG 660
AGACCTGCCC GCCCTCCTCG CAGCTCTGCT CTGTGTCCTC AGGAAGTCAC AGAGTCTACT 720
GAGGCAAGGA GAGGGTGATT CTTTCCCCAA ATCCCTTCTT CCCTGGTTCC CAAACCAAAG 780
ACAGCCTGCA GCCCTTTCTG CATGGGGTGC TCTGTTGACA GGCTTCCCAG ATCCCTGAGT 840
CTCTCTTTCC TTCCTCCTCG ATCTTTAGTT GTCCACGGTC AATTCAGTGC TTCCATTGGG 900
GGACAGTCCC CTCCGGGATG ACCTGATTCA CCTCCAGCCC AGGGAATGGA ATCTAGAGGA 960
ATACGTGGGG TGGGTCTGGA CAAGGAGCGG CAGGAATCAC CACCCATCTC CAGCTGTGGA 1020
GCCCTGTGGA GGGGAAGGGG AAGCTTGGGG TTCAGAGGGA ACTCTTCCAG GAGAGGGGTG 1080
CCCAGCGGAG GTAAAGATGA TAGAGGGTTG TGGGGGGTCT CTAGTTGAAT GTTTTGGCCC 1140
ATGACTTTGG AACATGGCTG GCAGCTTCCA GCAGAAGTCA CGCTCCCCAT CCCCAGGGG 1200
ACATAGGACC TTTTTCCTGC TTCCTGGTCA CTTTCAAAGA ACTATTTGCG CAATCTGTGG 1260
GTCTGTGGAT TCACGGGGCT TTCTGTGTGG GTGCTGCAGT TGCTTTTGTC TGCAGCAGCA 1320
GGACACATCT TTCCTCTTAC TCAGCCCTTT ATGGCCCATG GGGAACCTCCG TGGCTCAGGG 1380
AGAGCTGAAC TCCAGGGGTG TGACCTGGGA CAGGTGGGCC TGAGGTGCCC AGCTCAGGGC 1440
AGCCAGGTGG CTCATGGGCT GTAGTGAGCC AGCTCCCTGG GGGAAAAGGC TGTGGGCCGT 1500
TAGGACCATC CTCCAGGACA GGTGACCTCT ATGAGGTCAC CTACGGCTGT GGCCGTGCAG 1560
GCCTCCTTCC AGCCAGAGT GGCCAGTAG AGCAAGGCAG ACAGTGACCT CCACCCCCGC 1620
AGCCCTCTTA AAAGGCCAGT ACTCTTGGGG GTGGGGGGAG GGTTTAGAAA GCATTTGCCC 1680

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ATCTGCCTTT CTTTCCCCCA GCCCCACCC GCTTTGAATG TAGAGACCCG TGGGCACTTT 1740
TCCTTTTGTG GTGGGGGGTG CGGAGGAGGT ACCCCCACCC CTGGCACAGC CGCCTGGAAT 1800
GCAGGACTGT CACTGCTGTT CGGGTGATGA CCTCGTTGCC AAGCTCCTCC TGTCCCCTTG 1860
TTCTGGGGGC AGGCGCTGTG CTTCTGTGAG GTGGTTTAGC TTTTGCTTTC GAAGTGGCCA 1920
GCTGCGGCCA CCAGGTCTCA GCACAAGAGC GCTTCCTTTG CACAGAATGA GCTTCGAGCT 1980
TTGTTTCAGAC TAAATGAATG TATCTGGGAG GGGTCGGGGG CACGAGTTGA TTCCAAGCAC 2040
ATGCCTTTGC TGAGTGTGTG TGTGCTGGGA GAGTCAGAGT GGATGTAGAG CGCGGTTTTA 2100
TTTTTGTACT GACATTGGTA AGAGACTGTA TAGCATCTAT TTATTTAGAT GATTTATCTG 2160
GTAAATGAGG CAAAAAATT ATTAAAAATA CATTAAAGAT GATTTAAAAA AAAGACCAAA 2220
AAACCAAGAA ACCCAAAGCC CAAGAATGCG CGTAGCATCC AAAAAAAAAA GG 2272

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1060 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SPLNNOT04
- (B) CLONE: 1559131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99 :

GTCAACTTAG CGAGCGCAAC AGGCTGCCGC TGAGGAGCTG GAGCTGGTGG GGAAGTGGGCC 60
GCAATGGACA AGCTGAAGAA GGTGCTGAGC GGGCAGGACA CGGAGGACCG GAGCGGCCTG 120
TCCGAGGTTG TTGAGGCATC TTCATTAAGC TGGAGTACCA GGATAAAAGG CTTCAATTGCG 180
TGTTTTGCTA TAGGAATTCT CTGCTCACTG CTGGGTACTG TTCTGCTGTG GGTGCCCAGG 240
AAGGGACTAC ACCTCTTCGC AGTGTTTTAT ACCTTTGGTA ATATCGCATC AATTGGGAGT 300
ACCATCTTCC TCATGGGACC AGTGAAACAG CTGAAGCGAA TGTTTGAGCC TACTCGTTTG 360
ATTGCAACTA TCATGGTGCT GTTGTGTTTT GCACTTACCC TGTGTTCTGC CTTTTGGTGG 420
CATAACAAGG GACTTGCACT TATCTTCTGC ATTTTGCAGT CTTTGGCATT GACGTGGTAC 480
AGCCTTTCCT TCATACCATT TGCAAGGGAT GCTGTGAAGA AGTGTTTTGC CGTGTGTCTT 540
GCATAATTCA TGGCCAGTTT TATGAAGCTT TGGAAGGCAC TATGGACAGA AGCTGGTGGG 600
CAGTTTTGTA ACTATCTTCG AAACCTCTGT CTTACAGACA TGTGCCTTTT ATCTTGCAGC 660
AATGTGTTGC TTGTGATTCG AACATTTGAG GGTTACTTTT GGAAGCAACA ATACATTCTC 720

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GAACCTGAAT GTCAGTAGCA CAGGATGAGA AGTGGGTTCT GTATCTTGTG GAGTGGAATC 780
TTCCTCATGT ACCTGTTTCC TCTCTGGATG TTGTCCCACT GAATTCCCAT GAATACAAAC 840
CTATTGAGCA ACAGCACATA AGCCTTGGGT GCAAGTGATT CCCAGGTGGC AAAAGGCAGC 900
CCCATCAGAG ATCACGGGAG CAACAGTAAG GGACAGAGTT TTGGGGTCCA CTTGTCCCTC 960
AGCATGGAAG CCATCACCGT GGTCTGTCAT AGAGTGAGTC TGCTTCTACT CTGGCATCTG 1020
AGAACAAGTG ACTCTGCTTT AGACAAGCCC CTGGAGAGGG 1060

(2) INFORMATION FOR SEQ ID NO: 100:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 543 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
(A) LIBRARY: BLADNOT03
(B) CLONE: 1601473

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100 :

GCTCACAGTA GCCCGGCGGC CAGGGCAATC CGACCACATT TCACTCTCAC CGCTGTAGGA 60
ATCCAGATGC AGGCCAAGTA CAGCAGCACA AGGGACATGC TGGATGATGA TGGGGACACC 120
ACCATGAGCC TGCATTCTCA AGCCTCTGCC ACAACTCGGC ATCCAGAGCC CCGGCGCACA 180
GAGCACAGGG CTCCCTCTTC AACGTGGCGA CCAGTGGCCC TGACCCTGCT GACTTTGTGC 240
TTGGTGCTGC TGATAGGGCT GGCAGCCCTG GGGCTTTTGT GTAAGTCTGC GCTCTGACCT 300
GGGGGAGGAT CCTGTTTCCA AGTTTTTCAG TACTACCAGC TCTCCAATAC TGGTCAAGAC 360
ACCATTTCTC AAATGGAAGA AAGATTAGGA AATACGTCCC AAGAGTTGCA ATCTCTTCAA 420
GTCCAGAATA TAAAGCTTGC AGGAAGTCTG CAGCATGTGG CTGAAAAACT CTGTGCTGAG 480
CTGTATAACA AAGCTGGAGC ACACAGGTGC AGCCCTTGTA CAGAACAATG GAAATGGCAT 540
GGA 543

(2) INFORMATION FOR SEQ ID NO: 101:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2281 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(vii) IMMEDIATE SOURCE:
(A) LIBRARY: BRAITUT12
(B) CLONE: 1615809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101 :

AGCTGGCTCA CCTTCCAGAT TCACCTGCAG GAGCTGCTGC AGTACAAGAG GCAGAATCCA 60
GCTCAGTTCT GCGTTCGAGT CTGCTCTGGC TGTGCTGTGT TGGCTGTGTT GGGACACTAT 120
GTTCCAGGGA TTATGATTTC CTACATTGTC TTGTTGAGTA TCCTGCTGTG GCCCCTGGTG 180
GTTTATCATG AGCTGATCCA GAGGATGTAC ACTCGCCTGG AGCCCCTGCT CATGCAGCTG 240
GACTACAGCA TGAAGGCAGA AGCCAATGCC CTGCATCACA AACACGACAA GAGGAAGCGT 300
CAGGGGAAGA ATGCACCCCC AGGAGGTGAT GAGCCACTGG CAGAGACAGA GAGTGAAAGC 360
GAGGCAGAGC TGGCTGGCTT CTCCCCAGTG GTGGATGTGA AGAAAACAGC ATTGGCCTTG 420
GCCATTACAG ACTCAGAGCT GTCAGATGAG GAGGCTTCTA TCTTGAGAG TGGTGGCTTC 480
TCCGTATCCC GGGCCACAAC TCCGCAGCTG ACTGATGTCT CCGAGGATTT GGACCAGCAG 540
AGCCTGCCAA GTGAACCAGA GGAGACCCTA AGCCGGGACC TAGGGGAGGG AGAGGAGGGA 600
GAGCTGGCCC CTCCCGAAGA CCTACTAGGC CGTCCTCAAG CTCTGTCAAG GCAAGCCCTG 660
GACTCGGAGG AAGAGGAAGA GGATGTGGCA GCTAAGGAAA CCTTGTGCG GCTCTCATCC 720
CCCCCTCCACT TTGTGAACAC GCACTTCAAT GGGGCAGGGT CCCCCAAGA TGGAGTGAAA 780
TGCTCCCCCTG GAGGACCAGT GGAGACACTG AGCCCCGAGA CAGTGAGTGG TGGCCTCACT 840
GCTCTGCCCG GCACCCTGTC ACCTCCACTT TGCCTTGTG GAAGTGACCC AGCCCCCTCC 900
CCTTCCATTC TCCCACCTGT TCCCCAGGAC TCACCCAGC CCCTGCCTGC CCCTGAGGAA 960
GAAGAGGCAC TCACCACTGA GGACTTTGAG TTGCTGGATC AGGGGGAGCT GGAGCAGCTG 1020
AATGCAGAGC TGGGCTTGGA GCCAGAGACA CCGCCAAAAC CCCCTGATGC TCCACCCCTG 1080
GGGCCCCGACA TCCATTCTCT GGTACAGTCA GACCAAGAAG CTCAGGCCGT GGCAGAGCCA 1140
TGAGCCAGCC GTTGAGGAAG GAGCTGCAGG CACAGTAGGG CTTCTTGGCT AGGAGTGTG 1200
CTGTTTCCTC CTTTGCCTAC CACTCTGGGG TGGGGCAGTG TGTGGGGAAG CTGGCTGTG 1260
GATGGTAGCT ATTCCACCCT CTGCCTGCCT GCCTGCCTGC TGTCTGGGC ATGGTGCAGT 1320
ACCTGTGCCT AGGATTGGTT TTAAATTTGT AAATAATTTT CCATTGCGT TAGTGGATGT 1380
GAACAGGGCT AGGGAAGTCC TTCCCACAGC CTGCGCTTGC CTCCCTGCCT CATCTCTATT 1440
CTCATCCAC TATGCCCCAA GCCCTGGTGG TCTGGCCCTT TCTTTTCTCCT CCTATCTCA 1500
GGGACCTGTG CTGCTCTGCC CTCATGTCCC ACTTGGTTGT TTAGTTGAGG CACTTTATAA 1560
TTTTTCTCTT GTCTTGTGTT CCTTTCTGCT TTATTTCCCT GCTGTGTCCT GTCCTTAGCA 1620
GCTCAACCCC ATCCTTTGCC AGCTCCTCCT ATCCCGTGGG CACTGGCCAA GCTTTAGGGA 1680

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GGCTCCTGGT CTGGGAAGTA AAGAGTAAAC CTGGGGCAGT GGGTCAGGCC AGTAGTTACA 1740
CTCTTAGGTC ACTGTAGTCT GTGTAACTT CACTGCATCC TTGCCCCATT CAGCCCGGCC 1800
TTTCATGATG CAGGAGAGCA GGGATCCCGC AGTACATGGC GCCAGCACTG GAGTTGGTGA 1860
GCATGTGCTC TCTCTTGAGA TTAGGAGCTT CCTTACTGCT CCTCTGGGTG ATCCAAGTGT 1920
AGTGGGACCC CCTACTAGGG TCAGGAAGTG GACACTAACA TCTGTGCAGG TGTTGACTTG 1980
AAAAATAAAG TGTTGATTGG CTAGAACTGC TGCCTCCCTG ACTGTGAGCT GCCTTCCACA 2040
CCCTGCACTG CACTGTGTTT TCTCCTCACC CTTAACCTGC TTCACTCCAG TCTGTTCTGG 2100
CTGTTTATTA CTTGTTGCA AAACAGGGCC GAAGCAAGGA TTACCTTGAC AACCTAGCT 2160
TCTCCTTAGC CATCTTCCTT GACAGTGTGA TCTGTTAGT GAGATTTAGC ATGTGTGAAT 2220
AAAGTATATG CAGGAGGAAA TTGCTTTGTC TTCCAATCG GTAGAAATTC GAGACCTAGC 2280
C 2281

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 992 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNNOT19
- (B) CLONE: 1634813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102 :

GACAGCTTGG CCTACAGCCC GGCGGGCATC AGCTCCCTTG ACCCAGTGGA TATCGGTGGC 60
CCCGTTATTC GTCCAGGTGC CCAGGGAGGA GGACCCGCCT GCAGCATGAA CCTGTGGCTC 120
CTGGCCTGCC TGGTGGCCGG CTTCTGGGA GCCTGGGCCC CCGCTGTCCA CGCCCAAGGT 180
GTCTTTGAGG ACTGCTGCCT GGCCTACCAC TACCCCAT TG GGTGGGCTGT GCTCCGGCGC 240
GCCTGGACTT ACCGGATCCA GGAGGTGAGC GGGAGCTGCA ATCTGCCTGC TGCGATATTC 300
TACCTCCCCA AGAGACACAG GAAGGTGTGT GGGAACCCCA AAAGCAGGGA GGTGCAGAGA 360
GCCATGAAGC TCCTGGATGC TCGAAATAAG GTTTTGTCAA AGCTCCGCCA CAACACGCAG 420
ACCTTCCAAG CAGGCCCTCA TGCTGTAAAG AAGTTGAGTT CTGGAACTC CAAGTTATCA 480
TCATCCAAGT TTAGCAATCC CATCAGCAGC AGCAAGAGGA ATGTCTCCCT CCTGATATCA 540
GCTAATTCAG GACTGTGAGC CGGCTCATTT CTGGGCTCCA TCGGCACAGG AGGGGCCGGA 600
TCTTTCTCCG ATAAAACCGT CGCCCTACAG ACCCAGCTGT CCCACGCCT CTGTCTTTTG 660

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GGTCAAGTCT TAATCCCTGC ACCTGAGTTG GTCCTCCCTC TGCACCCCCA CCACCTCCTG 720
CCCGTCTGGC AACTGGAAAG AGGGAGTTGG CCTGATTTTA AGCCTTTTGC CGCTCCGGGG 780
ACCAGCAGCA ATCCTGGGCA GCCAGTGGCT CTTGTAGAGA AGACTTAGGA TACCTCTCTC 840
ACTTTCTGTT TCTTGCCGTC CACCCCGGGC CATGCCAGTG TGTCCCTCTG GGTCCCTCCA 900
AAACTCTGGT CAGTTCAAGG ATGCCCCTCC CAGGCTATGC TTTTCTATAA CTTTTAAATA 960
AACCTTGGGG GTTGATGGAG TCAAAAAAA AA 992

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1554 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: UTRSNOT06
- (B) CLONE: 1638407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103 :

TCGCCCAGGA GTCATCGGAC GCCAGAATCT GTGTCTCCAG AACGCTATAG CTATGGCACC 60
TCCAGCTCTT CAAAGAGGAC AGAGGGTAGC TGCCGTCGCC GTCGGCAGTC AAGCAGTTCT 120
GCAAATTCTC AGCAGGGTCA GTGGGAGACA GGCTCCCCC CAACCAAGCG GCAGCGGCGG 180
AGTCGGGGCC GGCCAGTGG TGGTGCCAGA CGGCGGCGGA GAGGGGCCCC AGCCGCACCC 240
CAGCAGCAGT CAGAGCCCGC CAGACCTTCC TCTGAAGGCA GGTGACACTG TGATGGGGAA 300
ACAGGCTCAG AGAGACATCC GGCTCCGGGT TCGAGCAGAG TACTGCGAGC ATGGGCCAGC 360
CTTGAGCAG GGCCTGGCAT CCCGGCGGCC CCAGGCGCTG GCGCGGCAGC TGGACGTGTT 420
TGGGCAGGCC ACCGCAGTGC TGCGCTCAAG GGACCTGGGC TCTGTGGTTT GTGACATCAA 480
GTTCTCAGAG CTCTCCTATC TGGACGCCTT CTGGGGCGAC TACCTGAGTG GCGCCCTGCT 540
GCAGGCCCTG CGGGGCGTGT TCCTGACTGA GGCCCTGCGA GAGGCTGTGG GCCGGGAGGC 600
TGTTGCGCTG CTGGTCAGTG TGGATGAGGC TGAATATGAG GCTGGCCGGC GCCGCCTGTT 660
GCTGATGGCG GAGGAAGGGG GGCGGCGCCC GACAGAGGCC TCCTGATCCA GGAATGGCAG 720
GATTGATCCC ACCTCCAAGT CTCCGGGCCA CCTTCTCCTG GGAGGACGAC CATCTCTACC 780
CCTAGAGGAC TGTCACCTA GCATCTTTGA GGACTGCGAC AGGACCGGGA CAGCAGGCCC 840
CTTGACAGCC CCTCCACAG GATGTGGGCT CTGAGGCCTA AACCATTTC AGCTGAGTTT 900
CCTTCCAGC CTCCTCCTAC CCCAGGTGT GCCCCCTTAG CCTCCGAGG CGGGGGCTGG 960

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GCCTGTATCT CAGAAGGGAG GGGCACAGCT ACACACTCAC CAAAGGCCCC CCTGCACATT 1020
GTATCTCTGA TCTTGGGCTG TCTGCACTGT CACAGGTGCA CACACTCGCT CATGCTCACA 1080
CTGCCCCTGC TGAGATCTTC CCTGGGCCTC TGCCCTGGCC TGCTTCCCAG CACACACTTC 1140
TTTGGCCTAA GGGCTTCTCT CTCAGGACCT CTAATTTGAC CACAACCAAC CTGGGCTTCA 1200
GCCACATCAG TGGGCACTGG AGCTGGGGTG CACATGGGGC CTGCTCACCT TGCCCACACA 1260
TCTCCAGCCA GCCAGGGCCC TGCCCAGCTT CAATTTACAG ACCTGACTCT CCTCACCTTC 1320
CCCCCTGCTG TCCAGAGCTG AACATAGACT TGCATTGGA TGTCACCTGG AGTGTCACAT 1380
GGGAGTGTTA TGGCAGCATC ATACCAAGGC CTACTGTTGC ACATGGGGCC AAAACCAAGTA 1440
AACAGCCACC TTCTTGAAA GGAATGCAA AGGCTTTGGG GGTGATGGAA AAGACCTTTT 1500
ACAAATGATA CCAATTAAAC TGCCCTGGAA AGGGCATAGG TGGGAAAAAA AAAA 1554

(2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSTUT08
- (B) CLONE: 1653112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104 :

GTCGCCGGGC TTGCGATGAA CTTCCGGCTG TCAAGCTCCC GGCCGGGCTG ACTCAAGCGG 60
AGGCGCGCGG AACAGTCGCC GAGGCGATTC CCGCCCAGGC TCCTGTAACC GCCAGGCAGC 120
GGCCCCGCCA TGTCCCAGCC CCGGACCCCA GAGCAGGCAC TGGATACACC GGGGGACTGC 180
CCCCCAGGCA GGAGAGACGA GGACGCTGGG GAGGGGATCC AGTGCTCCCA ACGCATGCTC 240
AGCTTCAGTG ACGCCCTGCT GTCCATCATC GCCACCGTCA TGATCCTGCC TGTGACCCAC 300
ACGGAGATCT CCCCAGAACA GCAGTTCGAC AGAAGTGTAC AGAGGCTTCT GGCAACACGG 360
ATTGCCGTCT ACCTGATGAC CTTTCTCATC GTGACAGTGG CCTGGGCAGC ACACACAAGG 420
TTGTTCCAAG TTGTTGGGAA AACAGACGAC ACACTTGCCC TGCTCAACCT GGCCTGCATG 480
ATGACCATCA CCTTCCTGCC TTACACGTTT TCGTTAATGG TGACCTTCCC TGATGTGCCT 540
CTGGGCATCT TCTTGTTCTG TGTGTGTGTG ATCGCCATCG GGGTCGTGCA GGCCTGATT 600
GTGGGGTACG CATTCCACTT CCCGCACCTG CTGAGCCCGC AGATCCAGCG CTCTGCCCAC 660
AGGGCTCTGT ACCGACGACA CGTCCTGGGC ATCGTCCTCC AAGGCCCGGC CCTGTGCTTT 720

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GCAGCGGCCA TCTTCTCTCT CTTCTTTGTC CCCTTGCTTT ACCTGCTGAT GGTGACTGTC 780
ATCCTCCTCC CCTATGTCAG CAAGGTCACC GGCTGGTGCA GAGACAGGCT CCTGGGCCAC 840
AGGGAGCCCT CGGCTCACCC AGTGGAAGTC TTCTCGTTTG ACCTCCACGA GCCACTCAGC 900
AAGGAGCGCG TGAAGCCTT CAGCGACGGA GTCTACGCCA TCGTGGCCAC GCTTCTCATC 960
CTGGACATCT GCGAAGACAA CGTCCCGGAC CCCAAGGATG TGAAGGAGAG GTTCAGCGGC 1020
AGCCTCGTGG CCGCCCTGAG TGCGACCGGG CCGCGCTTCC TGGCGTACTT CGGCTCCTTC 1080
GCCACAGTGG GACTGCTGTG GTTCGCCCAC CACTCACTCT TCCTGCATGT GCGCAAGGCC 1140
ACGCGGGCCA TGGGGCTGCT GAACACGCTC TCGCTGGCCT TCGTGGGTGG CCTCCCACTA 1200
GCCTACCAGC AGACCTCGGC CTTGCGCCGG CAGCCCCGCG ATGAGCTGGA GCGCGTGCCT 1260
GTCAGCTGCA CCATCATCTT CCTGGCCAGC ATCTTCCAGC TGGCCATGTG GACCACGGCG 1320
CTGCTGCACC AGGCGGAGAC GCTGCAGCCC TCGGTGTGGT TTGGCGGCCG GGAGCATGTG 1380
CTCATGTTCG CCAAGCTGGC GCTGTACCCC TGTGCCAGCC TGCTGGCCTT CGCCTCCACC 1440
TGCCTGCTGA GCAGGTTTCA TGTGGGCATC TTCCACCTCA TGCAGATCGC CGTGCCCTGC 1500
GCCTTCCTGT TGCTGCGCCT GCTCGTGGGC CTGGCCCTGG CCACCCTGCG GGTCCTGCGG 1560
GGCCTCGCCC GGCCCGAACA CCCCCGCCA GCCCCACGG GCCAGGACGA CCCACAGTCC 1620
CAGCTCCTCC CTGCCCCCTG CTAGCAGCCA CAGAGCCCAC TCCCAGCCGT CCTCACCAGA 1680
GATGGACCAG GGAGGACAGG ATGCTGGGCA GGGGAAGCCA AGTCACGGGC AGGCCGCAGT 1740
GGTTCTTGC TGGCCTGGTT TTATTTTCAT TGTGAAATAT CATGCTCTTA TTTAGTCTCT 1800
CA 1802

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTNOT09
- (B) CLONE: 1664634

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105 :

GTACCTCGGC TTATTTTATA AACAGGTACT GAAGGAAGCA GAGGCATGTG GAGGACTTCC 60
CCACCTCGTG CAGCTATTTG GGCCGTGGCA TCTGAAATTT CTTATTTTCA AGTCACCCCT 120
TTGATGACCT TGGCAGTGAA CTGCAGTCAT CTGTTTAGGC CTTTCCATGG CCCACGTCAA 180

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TGCCGGTATT TCTGTTTGTT GCACATTTGA TTTCTTGTT GTTGGCATTT AGAAGGCCCT 240
CGAGCCGCAC TGAGGGACTG AGCCTGGTGT ATATGGCAGC AAGACTGGAT GGTGGCTTTG 300
CAGCAGTCTC CAGAGCATTC CATGAGATCC GGGCTCGAAA TCCAGCATTT CAGCCACAAA 360
CTTTGATGGA CTTTGGCTCA GGTACTGGTT CTGTCACCTG GGCTGCTCAC AGTATTTGGG 420
GCCAGAGCCT ACGTGAATAT ATGTGTGTGG ACAGATCAGC TGCCATGTTG GTTTTGGCAG 480
AAAAACTACT GACAGGTGGT TCAGAATCTG GGGAGCCTTA TATTCCAGGT GTCTTTTCA 540
GACAGTTTCT ACCTGTATCA CCCAAGGTGC AGTTTGATGT AGTAGTGTCA GCTTTTTCCT 600
TAAGTGACCA GCTACTGACA TTTATACTTT CGTGTAATTC AAGTCTTCTG CATATTTTCC 660
CCTTTTGTGA ACAGGTACTG GTGGAGAATG GAACAAAAGC TGGGCACAGC CTTCTCATGG 720
ATGCCAGGGA TCTGGTCCTT AAGGGAAAAG AGAAGTCACC TTTGGACCCT CGACCTGGTT 780
TTGTCTTGC CCCGTGTCCC CATGAACCTC CTTGTCCCCA GTTGACCAAC CTGGCCTGTA 840
GCTTCTCACA GGCGTACCAT CCCATCCCCCT TCAGCTGGAA CAAGAAACCA AAGGAAGAAA 900
AGTTCTCTAT GGTGATCCTT GCTCGGGGGT CTCCAGAGGA GGCTCATCGC TGGCCCCGTA 960
TCACTCAGCC TGTCTTAAA CGGCCTCGCC ATGTGCATTG TCACTTGTGC TGTCCAGATG 1020
GGCACATGCA GCATGCTGTG CTCACAGCCC GCCGGCACGG CAGGTATGGG GGGTGTGACC 1080
AAAATCAGTG GGATGTGGCA GGAAGCTGCA GCCCACGCCA GCATCTGTTT CCACAGGGAT 1140
TTGTATCGTT GTGCCCCTGT CAGCTCCTGG GGAGATCTTT TACCTGTGCT TACTCCGTCT 1200
GCGTTTCCTC CATCTACGGC TCAGGATCCC TCTGAGAGTT GATGAGGATG TGTAACAAGT 1260
ATTTTCTTCT ATCGTGCCTG CCAGGGCTGA AGCTGCCTGG TATCCAGGAG GGAATGCTG 1320
GTATCCCCAT ATGTCTGTGT TTGTTTGAGA TTTTAAATAA TAAATAATAA ATTTTGAAG 1380
AATGAAAAAA AAAAA 1395

(2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1635 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSTUT10
- (B) CLONE: 1690990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106 :

CCCTCTTCCT TTTGCGCACG GAAGAACAAA TCACAACAAT CACACACCAG GACTGAATCC 60

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ATCAGCAGAT ACTGCCCTGT GGGAAAGGGCA GAGGAAAGAG AAGACAGACG GACTGACAGA 120
CACCACAGAG GAACAGGGGA GTTAGCCTGG GACCAATGGA GGAGAAGTAC GAACCCTGGG 180
AAAAAGACGT GTCAGATGAG AAAGTTCCGG AGAGTCCGAT GTCTCATCGC AGGTGTTACA 240
TCATCAGGGT TTGCCATTGG AATACTGAGT GGAGATGGGA AAGAGAAAAG TTAAGGGCTG 300
AAATGGGAGG GGAATGGGAA GAAAAAATGA GAGACAAGAG GGAAATAAGA AAAAACAAAG 360
AGAGCACAAA GACCAGTTTA GGAGAAAGGA CCAATGGGGA CAGTGGCAGA GTGGCGAGGT 420
AGGTGAAGGA CTGAGGCACA GCGTCCTGTT GTGGAGGGAG GAAAGGCAAG CGTTCCGAGG 480
TGGTGAAAAG GAAGGCCTGC TAGGCACGGT GGGGATGAAC GAGGATGCCA TGAGTCACAC 540
AAAAGACAGT GCTGGTGAGG CCCAGCCACA GGAGCCTCAG ATAACTTGGT AAAGGCATGT 600
CTCCCATTTG GGAAGTATG TTCCTAAGAT CCGCACTGAC GCTGCTCAGC CGGTCCATCA 660
CACAGCAAAG GCGTGAGGAA GGGTCACTGC CCAGCTGGAC TCCAGGGTGG TCCACGCATG 720
ACAGTCACAC CGAACCTTCA TGAGGATGTG AACTGTTGGC TCCAATTTAC CATTCCCAGC 780
AATTCCACTC AGATATTTGT ATACTAATGT TCACAGCAGC GTGAACTCCA CAGCAGGTGG 840
AGTAATGTTT CATTGTGTGC ATATGCCACA TTTTGTTTAT CCATTCATCT GTTGATGCAC 900
ATTTTCGGTTG TTCCACCTT TGGGCTATTA TTAATAATGC TGCTGTGAAC ATTCCCAAGA 960
GAAATAGGAA GACGGCTTTG CTAAGAACTA AAAAAGGGAT GGACAACAAG GGCATATACC 1020
CAGGGGCAGT GTTCTATCAT GACAGCTTTA CTGAGAGCAG AGTAGTTCTG CTCAGAATCA 1080
GAACACTTGT TCCCTATAGC CCCCCTGATT GCCCCACAAC CACCACCGCA TACTCCCCTT 1140
TTCCCAACCA TGGGCAGCAG ATTGAGCTAT TAACAGAAGT GTCCTTTTCGC TGGATTTCTC 1200
AACCCTTTCC TCATCGTCCA CATAGAGAAA CAGTAACAGA TTGCTACTCA CCCAACACCC 1260
AGGTCAAGTC CAATGCAGGT AGGAATAACA GCAAATCCTT CAATTTCTTG ATTCTGCTCT 1320
TAAAAATCTT AACAGAGGCT TCCAGGTTCT GAAAATATTT TCTGCATAAA CGTGTGACAC 1380
TCCATCACGA AACTCCCTTT GGTTATCTGC TTAAACTTAT CGCAAATGTC TGGAACGCTG 1440
GTGGCTTCCA AAATCAACTC CTGGTGCTGC TTAATTAAGG TCAGGGCCAC CCGGAAGATA 1500
ATCTTCGAGC CTTTCGTTAAA CAAACAGTCC CAGATCCGAA GCACTGTCTC CACGGGCAAG 1560
ATGTCCACAA ACAGGCAGAT GAACCAGCGG GACACCAGCA GCGTCCACAG CACACCGAGA 1620
CGCTCCATCA GGGGG 1635

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 1485 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: DUODNOT02
(B) CLONE: 1704050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107 :

TTTTTGGTCC CGNCNAAAGN CCNAAAACCC GGNACCCGGG AAGCCNCCCC AANNCNAAAN 60
TTCCCAGTTN GAANCCCGAA GGNAAAACCC CGGAAAAGNA NNCNGCCCN AAANTTCNCG 120
GGCNAAAACC CGGCCNTTTT TTCCCCCCCCG GCGGCCCGTT TTGGGCCCCN GANTTTCCAT 180
TTAAANTNCC NAGNCTTGGG CAACCTAACC AGGNTTTTCC CCCAANCTGG AAAAAGCCGG 240
GCCAAGTTGA GCCGCACCCG CCCCAGAAGT TCAAGGGCCC CCGGCCTCCT GCGCTCCTGC 300
CGCCGGGACC CTCGACCTCC TCAGAGCAGC CGGCTGCCGC CCCGGGAAGA TGGCGAGGAG 360
GAGCCGCCAC CGCCTCCTCC TGCTGCTGCT GCGCTACCTG GTGGTCGCCC TGGGCTATCA 420
TAAGGCCTAT GGGTTTTCTG CCCCAAAAGA CCAACAAGTA GTCACAGCAG TAGAGTACCA 480
AGAGGCTATT TTAGCCTGCA AAACCCCAAA GAAGACTGTT TCCTCCAGAT TAGAGTGGAA 540
GAAACTGGGT CGGAGTGTCT CCTTTGTCTA CTATCAACAG ACTCTTCAAG GTGATTTTAA 600
AAATCGAGCT GAGATGATAG ATTTCAATAT CCGGATCAAA AATGTGACAA GAAGTGATGC 660
GGGGAAATAT CGTTGTGAAG TTAGTGCCCC ATCTGAGCAA GGCCAAAACC TGGAAGAGGA 720
TACAGTCACT CTGGAAGTAT TAGTGGCTCC AGCAGTTCCA TCATGTGAAG TACCCTCTTC 780
TGCTCTGAGT GGAAGTGTGG TAGAGCTACG ATGTCAAGAC AAAGAAGGGA ATCCAGCTCC 840
TGAATACACA TGGTTTAAGG ATGGCATCCG TTTGCTAGAA AATCCCAGAC TTGGCTCCCA 900
AAGCACCAAC AGCTCATACA CAATGAATAC AAAAAGTGA ACTCTGCAAT TTAATACTGT 960
TTCCAAACTG GACACTGGAG AATATTCCTG TGAAGCCCGC AATTCTGTTG GATATCGCAG 1020
GTGTCCTGGG AAACGAATGC AAGTAGATGA TCTCAACATA AGTGGCATCA TAGCAGCCGT 1080
AGTAGTTGTG GCCTTAGTGA TTTCCGTTTG TGGCCTTGGT GTATGCTATG CTCAGAGGAA 1140
AGGCTACTTT TCAAAGAAA CCTCCTTCCA GAAGAGTAAT TCTTCATCTA AAGCCACGAC 1200
AATGAGTGAA AATGATTTCA AGCACACAAA ATCCTTTATA ATTTAAAGAC TCCACTTTAG 1260
AGATACACCA AAGCCACCGT TGTTACACAA GTTATTAAAC TATTATAAAA CTCTGCTTTG 1320
TCCGACATTT GCAAAGAGGT ACACGAGGAA ATGGAATTGG TATTTCAATTT TAATTTTCAT 1380
GACTACTAAC TCACCTGAAC TTGCTATTTT AAACAAATAG TTCTGTGCGAC ACCTAAAATA 1440
TAATCTGGCT TCTTGTGTCT GGACTAAGTT AAAAGAATTA AAATA 1485

(2) INFORMATION FOR SEQ ID NO: 108:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 810 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
 (A) LIBRARY: PROSNOT16
 (B) CLONE: 1711840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108 :

CGAGTGAGCG CGCGGCGGCC CCTGGTCCGC CCGGCCGCGG CCGATCTAGG GGCTGGGGGC 60
 TGGAGGCGGG GGTGGGGGTC TGAGCTGCGT CCTGGGCTCG AGGCGTCCCC CGGGGAGTCG 120
 CCTCTTAGCG GTGCGTCCGG GCTAGCGGCG AGGGGCCGCC CCAAGTCTTC CCACCGCCGC 180
 CACCTTAGCA GCCCGACTTG GGCCTGGAA AGTGGAGCAC GCGGAGGTGG GAGGGCCCTG 240
 CACGCGGCCC CCGGTGGGGA AGGGGACGGG CCAGGGATTC AGACTCGGGC TCTCCCCTCA 300
 GGATGCAGCA CCGAGGCTTC CTCCTCCTCA CCCTCCTCGC CCTGCTGGCG CTCACCTCCG 360
 CGGTCGCCAA AAAGCAAGAT AAGGTGAAGA AGGGCGGCCC GGGGAGCGAG TGCGCTGAGT 420
 GGGCCTGGGG GCCCTGCACC CCCAGCAGCA AAGGATTGCG GGCAGTGGGT TTTCCGCGAG 480
 GGCCACCTTG GGGGGGCCCA AGAACCCAAC CGGCAGTCCT GGTGAAAGG GTTGCCCCTG 540
 GAAAGTTGGA AAGAAAGGAG TTTTGGGCAC CCGGACTTTG GAAAGTTGGC CAAATTTTTT 600
 GGAAGAAAAC TTGGCGGGTC TGCCGGTCCG TTAAATGGGG GAGGGGACAA AAGAATTGAA 660
 AGCCGAAAAA ATGCTTTCTC CGCCGCCAAG AGAGGTCGAA CCCGCGTCTG GCAAGAAGAG 720
 AAAAGGGCGC GCCCACACTG TTAACAACAA TATGGCGCCT GAACAGTTGG TGGCACCACA 780
 GGGGGAGGGA GACACATACT TGCGCGCGGT 810

(2) INFORMATION FOR SEQ ID NO: 109:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1064 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109 :

TTCTTGGGGC TCCGGGGCGC GGAGAAGCTG CATCCAGAG GAGCGCGTCC AGGAGCGGAC 60

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CCGGGAGTGT TTCAAGAGCC AGTGACAAGG ACCAGGGGCC CAAGTCCCAC CAGCCATGCA 120
GACCTGCCCC CTGGCATTCC CTGGCCACGT TTCCCAGGCC CTTGGGACCC TCCTGTTTTT 180
GGCTGCCTCC TTGAGTGCTC AGAATGAAGG CTGGGACAGC CCCATCTGCA CAGAGGGGGT 240
AGTCTCTGTG TCTTGGGGCG AGAACACCGT CATGTCCTGC AACATCTCCA ACGCCTTCTC 300
CCATGTCAAC ATCAAGCTGC GTGCCCACGG GCAGGAGAGC GCCATCTTCA ATGAGGTGGC 360
TCCAGGCTAC TTCTCCCGGG ACGGCTGGCA GCTCCAGGTT CAGGGAGGCG TGGCACAGCT 420
GGTGATCAAA GGCGCCCGGG ACTCCCATGC TGGGCTGTAC ATGTGGCACC TCGTGGGACA 480
CCAGAGAAAT AACAGACAAG TCACGCTGGA GGTTCAGGT GCAGAACCCC AGTCCGCCCC 540
CGACACTGGG TTCTGGCCTG TGCCAGCGGT GGTCACTGCT GTCTTCATCC TCTTGGTCGC 600
TCTGGTCATG TTCGCCTGGT ACAGGTGCCG CTGTTCCCAG CAACGCCGGG AGAAGAAGTT 660
CTTCCTCCTA GAACCCCAAG TGAAGGTGCG AGCCCTCAGA GCGGGAGCCC AGCAGGGCCT 720
GAGCAGAGCC TCCGCTGAAC TGTGGACCCC AGACTCCGAG CCCACCCCAA GGCCGCTGGC 780
ACTGGTGTTT AAACCCTCAC CACTTGGAGC CCTGGAGCTG CTGTCCCCC AACCCTTGTT 840
TCCATATGCC GCAGACCCAT AGCCGCCTGC AAGGAAGAGA GGACACAGGA GTAGCCACCC 900
TGAGTGCCGA CCTTTGGTGG CGGGGGCCTG GGTCTCTCGT CCCACCCGG AAGGGCACAA 960
GACACCGGGC TTTGCTTGGC AAGGCTTGGG GCCTCTTGTG GTCAACCCAG TTCCCTTGGG 1020
TGCCGTTGCA GAACCCCTTA GCCCCTTCCA ACGTCGACCA GGTT 1064

(2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1031 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110 :

AGTTCCTGCA GGTGCCGGCG GTGACGCGGG CTTACACCGC AGCCTGTGTC CTCATCCACC 60
GCCGCGGTGC AGCTGGAGCT CCTCAGCCCC TTTCAACTCT ACTTCAACCC GCACCTTGTG 120
TTCCGGAAGT TCCAGGTGAG GCCGCCTCGC GCCGCGCACC TGGGGCCCGA CCCACCCACC 180
CCGCACCTGA CCGCCCGTCC CCCGTAGGTC TGGAGGCTCG TCACCAACTT CCTCTTCTTC 240
GGGCCCCCTG GATTCACTT CTTCTTCAAC ATGCTCTTCG TGTATCCTGC GCCTGCGGAC 300
ACGGGCTGGG TGGAGGGCAG GCCGGCCGGG CTGGGAGAGA GGCCGGGACG GGGAACTGA 360

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GGCCCCGCCT GGTGGCACTT CCTATACCGA CGCCGTAGGT TCCGCTACTG CCGCATGCTG 420
GAAGAGGGCT CCTTCCGCGG CCGCACGGCC GACTTCGTCT TCATGTTTCT CTTCGGGGGC 480
GTCCTTATGA CCGTATCCTT CCCGCAGGCT CTGGAACCTC GGGCTAGGGC GCCTCGGCGT 540
CCAGCCTGTG TTGGTCTGCG GGCCAACACA GCCATGCCAG AGAGGGACAC AGTCGCTGTC 600
TCCAGCTTAG CACCGTTCCT GCCTTGGGCG CTCATGGGCT TCTCGCTGCT GCTGGGCAAC 660
TCCATCCTCG TGGACCTGCT GGGGATTGCG GTGGGCCATA TCTACTACTT CCTGGAGGAC 720
GTCTTCCCCA ACCAGCCTGG AGGCAAGAGG CTCCTGCAGA CCCCTGGCTT CCTAAAGCTG 780
CTCCTGGATG CCCCTGCAGA AGACCCCAAT TACCTGCCCC TCCCTGAGGA ACAGCCAGGA 840
CCCCATCTGC CACCCCCGCA GCAGTGACCC CCACCCAGGG CCAGGCCTAA GAGGCTTCTG 900
GCAGCTTCCA TCCTACCCAT GACCCCTACT TGGGGCAGAA AAAACCCATC CTAAAGGCTG 960
GGCCCATGCA AGGGCCCACC TGAATAAACA GAATGAGCTG CAAAAAAAAA AAAAAAGGGC 1020
GGCCGTCGCG A 1031

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSTUT12
- (B) CLONE: 1812375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111 :

GCTGGATAAG ACACCAGGGG AGTCACTACA TGGTTACCGC ATCTGTATCC AGGCCATCCT 60
GCAAGACAAG CCCAAGATTG CCACGGCAAA CCTAGGCAAG TTCCTGGAAC TGCTGAGGTC 120
CCACCAGAGC CGACCAGCAA AGTGTCTCAC CATCATGTGG GCCCTGGGTC AAGCAGGTTT 180
TGCCAACCTC ACCGAGGGAC TGAAAGTGTG GCTGGGGATC ATGCTGCCTG TGCTGGGCAT 240
CAAGTCTCTG TCTCCCTTTG CCATCACATA CCTGGATCGG CTGCTCCTGA TGCATCCCAA 300
CCTTACCAAG GGCTTCGGCA TGATTGGCCC CAAGGACTTC TTCCCACTTC TGGACTTTGC 360
CTATATGCCG AACAACTCCC TGACACCCAG CCTGCAGGAG CAGCTGTGTC AGCTCTACCC 420
CCGACTGAAA ATGCTGGCAT TTGGAGCAAA GCCGGATTCC ACCCTGCATA CCTACTTCCC 480
TTCTTTTCTG TCCAGAGCCA CCCCTAGCTG TCCCCCTGAG ATGAAGAAAG AGCTCCTGAG 540
CAGCCTGACT GAGTGCCTGA CGGTGGACCC CCTCAGTGCC AGCGTCTGGA GGCAGCTGTA 600

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CCCTAAGCAC CTGTCACAGT CCAGCCTTCT GCTGGAGCAC TTGCTCAGCT CCTGGGAGCA 660
GATTCCCAAG AAGGTACAGA AGTCTTTGCA AGAAACCATT CAGTCCCTCA AGCTTACCAA 720
CCAGGAGCTG CTGAGGAAGG GTAGCAGTAA CAACCAGGAT GTCGTCACCT GTGACATGGC 780
CTGCAAGGGC CTGTTGCAGC AGGTTTCAGG TCCTCGGCTG CCCTGGACGC GGCTCCTCCT 840
GTTGCTGCTG GTCTTCGCTG TAGGCTTCCT GTGCCATGAC CTCCGGTCAC ACAGCTCCTT 900
CCAGGCCTCC CTTACTGGCC GGTTGCTTCG ATCATCTGGC TTCTTACCTG CTAGCCAACA 960
AGCGTGTGCC AAGCTCTACT CCTACAGTCT GCAAGGCTAC AGCTGGCTGG GGGAGACACT 1020
GCCGCTCTGG GGCTCCCACC TGCTCACCGT GGTGCGGCCC AGCTTGCAGC TGGCCTGGGC 1080
TCACACCAAT GCCACAGTCA GCTTCCTTTC TGCCCACTGT GCCTCTCACC TTGCGTGGTT 1140
TGGTGACAGT CTCACCAGTC TCTCTCAGAG GCTACAGATC CAGCTCCCCG ATTCCGTGAA 1200
TCAGCTACTC CGCTATCTGA GAGAGCTGCC CCTGCTTTTC CACCAGAATG TGCTGCTGCC 1260
ACTGTGGCAC CTCTTGCTTG AGGCCCTGGC CTGGGCCCAG GAGCACTGCC ATGAGGCATG 1320
CAGAGGTGAG GTGACCTGGG ACTGCATGAA GACACAGCTC AGTGAGGCTG TCCACTGGAC 1380
CTGGCTTTGC CTACAGGACA TTACAGTGGC TTTCTTGAC TGGGCACTTG CCCTGATATC 1440
CCAGCAGTAG GCCCTGCCTT CCTGGCCACT GATTTCCTGCA TGGGTAGACC ATCCAAGACT 1500
GCAGCGGGTA GAAGGTGGCA GTTCTTCATG GGAGTCTTTT TAACTTGGTG CCTGAGTTCT 1560
CTCCTAGGCA AGTGGCCAGT TGCCTCCACC TCAGTTCTTC CATCTTTGGT GGGGACAGGG 1620
CCCAGCAGCA TCTCAGCCTC CTACCCACAA TTCCACTGAA CACTTTTCTG GCCCTACTGC 1680
ACATGGCCCC CAGCCTCCAT CCTTGTGCTG GTAGCCTCTC ACAACTCCGC CCTTGCCCTC 1740
TGCCTTCCAC TTCCTTCCAT CTCATTTCTA AACCCCAAAC AGCTCATCTC TAAAAAGATA 1800
GAACTCCCAG CAGGTGGCTT CTGTGTTCTT CTGACAAATG ATTCCTGCTT CTCCAGACTT 1860
TAGCAGCCTC CTGTTCCCAT TCTTGGTCAC AGCTCTAGCC ACAGCAGAAG GAAAGGGGCT 1920
TCCAGAAGAA TATAGCACCG CATTGGGAAA CAGCAGCCTC ACCTCCACCT GAAGCCTGGG 1980
TGTGGCTGTC AGTGGACATG GGGAGCTGGA TGGAATGCC TCTCACTTCA AAATGCCCAG 2040
CCTGCCCCAA ATGCCTCTAA GCCCCTCCCT GTCCCCTCCC TTGTAGTCCT ACTTCTTCCA 2100
ACTTTCCATT CCCCATCATG CTGGGGGTCT TGGTCACAAG GCTCAGCTTC TCTCCACTGT 2160
CCATCCCTCC TATCATCTGT AGAGCAGAGC ACAGGCAGTT GTGTGCCTTG GGCCCAGGGA 2220
ACCCTCCATC AACCTGAGAC AGGACTCAGT ATATGGTTCT TGGGTATGCC CTACCAGGTG 2280
GAATAAAGGA CACAGATTTG AAAAAAAAAA AAAAAA 2316

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(2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1169 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNOT20
- (B) CLONE: 1818761

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112 :

AGCAAGGAGC CAGAGGCCAT GCAGTGGCTC AGGGTCCGTG AGTCGCCTGG GGAGGCCACA 60
GGACACAGGG TCACCATGGG GACAGCCGCC CTGGGTCCCC TCTGGGCAGC GCTCCTGCTC 120
TTTCTCCTGA TGTGTGAGAT CCCTATGGTG GAGCTCACCT TTGACAGAGC TGTGGCCAGC 180
GGCTGCCAAC GGTGCTGTGA CTCTGAGGAC CCCCTGGATC CTGCCCATGT ATCCTCAGCC 240
TCTTCCTCCG GCCGCCCCCA CGCCCTGCCT GAGATCAGAC CCTACATTAA TATCACCATC 300
CTGAAGGGTG ACAAAGGGGA CCCAGGCCCA ATGGGCCTGC CAGGGTACAT GGGCAGGGAG 360
GGTCCCCAAG GGGAGCCTGG CCCTCAGGGC AGCAAGGGTG ACAAGGGGGA GATGGGCAGC 420
CCCGGCGCCC CGTGCCAGAA GCGCTTCTTC GCCTTCTCAG TGGGCCGCAA GACGGCCCTG 480
CACAGCGGCG AGGACTTCCA GACGCTGCTC TTCGAAAGGG TCTTTGTGAA CCTTGATGGG 540
TGCTTTGACA TGGCGACCGG CCAGTTTGCT GCTCCCCTGC GTGGCATCTA CTTCTTCAGC 600
CTCAATGTGC ACAGCTGGAA TTACAAGGAG ACGTACGTGC ACATTATGCA TAACCAGAAA 660
GAGGCTGTCA TCCTGTACGC GCAGCCCAGC GAGCGCAGCA TCATGCAGAG CCAGAGTGTG 720
ATGCTGGACC TGGCCTACGG GGACCGCGTC TGGGTGCGGC TCTTCAAGCG CCAGCGCGAG 780
AACGCCATCT ACAGCAACGA CTTGACACC TACATCACCT TCAGCGGCCA CCTCATCAAG 840
GCCGAGGACG ACTGAGGGCC TCTGGGCCAC CCTCCCGGCT GGAGAGCTCA GGTGCTGGTC 900
CCGTCCCCTG CAGGGCTCAG TTTGCACTGC TGTGAAGCAG GAAGGCCAGG GAGGTCCCCG 960
GGGACCTGGC ATTCTGGGGA GACCCTGCTT CTATCTTGGC TGCCATCATC CCTCCCAGCC 1020
TATTTCTGCT CCTCTCTTCT CTCTTGACC TATTTTAAGA AGCTTGCTAA CCTAAATATT 1080
CTAGAACTTT CCCAGCCTCG TAGCCCAGCA CTTCTCAAAC TTGGAAATGC ATGCGAATCA 1140
CCCGGGGTTC GTGTTAAATG CAGATTCTG 1169

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 1530 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: GBLATUT01
(B) CLONE: 1824469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113 :

TCACAGACTG CGGAGTGGGT CAGGGGCTGC GAGGGCTGCC CCAAGTCCTA CCGGGTTTGC 60
ACGGGCGCGC CCGGCTCCGC CCGCAAGTGC GCCTTCCTGA CTTACTGCTG GGTGCGCGGG 120
GCTGGGGGTG CGAGTACCAC CCCTGAAGTC TCTTCCTGGG CGACCTCCGG GGCCTCATTC 180
TAGGCCCTCCT TAAAGAGAAG GATCTAAATT AGGAAAAGGA AGTGCCCTTA TCCACGACCA 240
AGCTCTTCCA CCTGCGGAGC TCGCTTAGTC TGCACCTCAA CCGTGCGGAA AGTGA CTGCC 300
CTGTTTACTG AGGAAAAACT GGGGCTCAGA AAGATACCAT GAGTAGTTTG AAACAGGAAC 360
AAAATCTTCT GAAAGCTCGG AGCAGAAGCC TTTTGGTCA ACATGGAGGA AAAAAGACGG 420
CGAGCCCGAG TTCAGGGAGC CTGGGCTGCC CCTGTAAAA GCCAGGCCAT TGCTCAGCCA 480
GCTACCACTG CTAAGAGCCA TCTCCACCAG AAGCCTGGCC AGACCTGGAA GAACAAAGAG 540
CATCATCTCT CTGACAGAGA GTTTGTGTTT AAAGAACCTC AGCAGGTAGT ACGTAGAGCT 600
CCTGAGCCAC GAGTGATTGA CAGAGAGGGT GTGTATGAAA TCAGCCTGTC ACCCACAGGT 660
GTATCTAGGG TCTGTTTGTA TCCTGGCTTT GTTGACGTGA AAGAAGCTGA CTGGATATTG 720
GAACAGCTTT GTCAAGATGT TCCCTGGAAA CAGAGGACCG GCATCAGAGA GGATATAACT 780
TATCAACAAC CAAGACTTAC AGCATGGTAT GGAGAACTTC CTTACACTTA TTCAAGAATC 840
ACTATGGAAC CAAATCCTCA CTGGCACCCCT GTGCTGCGCA CACTAAAGAA CCGCATTGAA 900
GAGAACACTG GCCACACCTT CAACTCCTTA CTCTGCAATC TTTATCGCAA TGAGAAGGAC 960
AGCGTGGACT GGCACAGTGA TGATGAACCC TCACTAGGGA GGTGCCCCAT TATTGCTTCA 1020
CTAAGTTTGT GTGCCACACG CACATTTGAG ATGAGAAAAG AGCCACCACC AGAAGAGAAT 1080
GGAGACTACA CATATGTGGA AAGAGTGAAG ATACCCTTGG ATCATGGTAC CTTGTTAATC 1140
ATGGAAGGAG CGACACAAGC TGA CTGGCAG CATCGAGTGC CCAAAGAATA CCACTCTAGA 1200
GAACCGAGAG TGAACCTGAC CTTTCGGACA GTCTATCCAG ACCCTCGAGG GGCACCCTGG 1260
TGACGTCAGA GCTTTGAGAG AGAAGCTTCA CTGAAACGGA GCAAACCTTC CACTGAGAAG 1320
CCACTTCAAG AGGCTGGTGC TGCTAGATCT CATGATGTGG CTGTTGGGAA GATGGTGGGG 1380
TTTGTGTGCC AGCTTGAGT CCTATTAAAT GAAAGCCAGC AACTCATGTT GGTAATAGGT 1440
CTACTGTGGG AACAGTTATC CCTAACCACA GCTCAAAATC GCTATCATCT TTAGGCAAAT 1500

TAAAATCTAT GTGGCAGTGA AAAAAAAAAA

1530

(2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNOT19
- (B) CLONE: 1864292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114 :

AGCTCGTACC CCTCGAGTGA AATTCTGAAA TGAAGATGGA GGAGGCAGTG GGAAAAGTTG 60
AAGAACTCAT TGAGTCCGAA GCCCCACCAA AAGCATCTGA ACAAGAGACA GCCAAGGAGG 120
AAGATGGATC TGTAGAACTG GAATCTCAAG TTCAGAAAAGA TGGTGTAGCG GATTCTACAG 180
TTATTTCTTC AATGCCCTGC TTGTTGATGG AACTGAGAAG GGACTCTTCT GAGTCTCAGT 240
TAGCATCCAC AGAGAGTGAC AAGCCTACAA CTGGCCGAGT TTATGAGAGT GACCCCTCTA 300
ATCACTGCAT GCTTTCCCCT TCCTCTAGTG GTCACCTGGC TGATTTCAGAT ACGTTGTCTT 360
CCGCAGAAGA GAATGAACCC TCTCAGGCAG AAACGGCGGT AGAAGGAGAC CCTTCAGGAG 420
TGTCTGGTGC CACAGTTGGG CGCAAGTCTA GGCGGTCCCG ATCTGAAAGT GAAACTTCCA 480
CTATGGCTGC CAAGAAAAAC CGGCAATCCA GTGATAAACA GAATGGCCGA GTCGCCAAGG 540
TTAAAGGTCA TCGGAGCCAA AAGCACAAGG AGAGGATCAG GCTACTGAGG CAGAAACGGG 600
AGGCTGCTGC AAGGAAGAAA TATAACCTGC TGCAGGACAG TAGTACCAGT GATAGTGACC 660
TGACTTGTGA CTCAAGCACG AGCTCATCAG ATGATGATGA AGAGGTTTCA GGGAGCAGCA 720
AGACAATCAC TGCAGAGATA CCAGATGGAC CTCCAGTTGT AGCTCATTAT GATATGTCTG 780
ACACCAACTC TGACCCAGAA GTGGTAAATG TGGACAATTT ATTGGCGGCT GCAGTAGTTC 840
AAGAGCACAG TAATTCTGTA GGCGGCCAGG ACACAGGAGC TACCTGGAGG ACCAGCGGGC 900
TTCTAGAGGA GCTGAATGCA GAGGCAGGTC ATTTGGATCC AGGATTCCTA GCAAGTGACA 960
AAACATCTGC TGGCAATGCG CCACTCAATG AAGAAATTAA CATTGCGTCT TCAGATAGTG 1020
AAGTAGAGAT TGTGGGAGTT CAGGAACATG CAAGGTGTGT TCATCCTCGA GGTGGTGTGA 1080
TTCAGAGTGT TTCTTCATGG AAGCATGGCT CGGGCACGCA GTATGTTAGC ACCAGGCAAA 1140
CACAGTCATG GACTGCTGTG ACTCCCCAGC AGACTTGGGC TTCACCAGCA GAAGTTGTTG 1200
ACCTTACCTT GGATGAGGAT AGCAGGCGTA AATACCTACT GTAATACAAT GTCAGTGTGT 1260

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TTCCTCTGCA CTGTTCCCTT CCACTTCCTC ATCCTCTTTG TGACATGGAA GTTCATTGTC 1320
ATAGGGGTAC GGAGCT 1336

(2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1742 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THP1NOT01
- (B) CLONE: 1866437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115 :

GGCCCGCCCC CTCCCCGCCC GCCTTCCCGG TGACCTTCAG GGGCCCGGGT GGCGGGCGCA 60
GGCCCCCTGCG GCGGCGGCGG GATGTTTCGTG CAGGAGGAGA AGATCTTCGC GGGCAAGGTG 120
CTGCGGCTGC ACATCTGCGC GTCCGACGGC GCCGAGTGGC TGGAGGAGGC CACCGAGGAC 180
ACCTCGGTGG AGAAGCTCAA GGAGCGCTGC CTCAAGCACT GTGCTCATGG GAGCTTAGAA 240
GATCCCCAAA GTATAACCCA TCATAAATTA ATCCACGCTG CCTCAGAGAG GGTGCTGAGT 300
GATGCCAGGA CCATCCTGGA AGAGAACATC CAGGACCAAG ATGTCCTATT ATTGAAAAAA 360
AAGCGTGCTC CATCACCCT TCCAAGATG GCTGATGTCT CAGCAGAAGA AAAGAAAAAA 420
CAAGACCAGA AAGCTCCAGA TAAAGAGGCC ATACTGCGGG CCACCGCCAA CCTGCCCTCC 480
TACAACATGG ACCGGGCGCG GGTCCAGACC AACATGAGAG ACTTCCAGAC AGAACTCCGG 540
AAGATACTGG TGTCTCTCAT CGAGGTGGCG CAGAAGCTGT TAGCGCTGAA CCCAGATGCG 600
GTGGAATTGT TTAAGAAGGC GAATGCAATG CTGGACGAGG ACGAGGATGA GCGTGTGGAC 660
GAGGCTGCCC TGCGGCAGCT CACGGAGATG GGCTTTCCGG AGAACAGAGC CACCAAGGCC 720
CTTCAGCTGA ACCACATGTC GGTGCCTCAG GCCATGGAGT GGCTAATTGA ACACGCAGAA 780
GACCCGACCA TAGACACGCC TCTTCCTGGC CAAGCTCCCC CAGAGGCCGA GGGGGCCACA 840
GCAGCTGCCT CCGAGGCTGC CGCGGGAGCC AGCGCCACCG ATGAGGAGGC CAGAGATGAG 900
CTGACGGAAA TCTTCAAGAA GATCCGGAGG AAAAGGGAGT TTCGGGCTGA TGCTCGGGCC 960
GTCATTTCCC TGATGGAGAT GGGGTTTCGAC GAGAAAGAGG TGATAGATGC CCTCAGAGTG 1020
AACAACAACC AGCAGAATGC CGCGTGCGAG TGGCTGCTGG GGGACCGGAA GCCCTCTCCG 1080
GAGGAGCTGG ACAAGGGCAT CGACCCCGAC AGTCCTCTCT TTCAGGCCAT CCTGGATAAC 1140
CCGGTGGTGC AGCTGGGCCT GACCAACCCG AAAACATTGC TAGCATTTGA AGACATGCTG 1200

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GAGAACCCAC TGAACAGCAC CCAGTGGATG AATGATCCAG AAACGGGGCC TGTCATGCTG 1260
CAGATCTCTA GAATCTTCCA GACACTAAAT CGCACGTAGG TGGCGTTGTT CCACTCGGCT 1320
ATCAGGCCAC AGCAGCCCCC TGGTGC GGCC CGAGACCGGG CAGAGTGGAC CTCACCTGGA 1380
AACTCACCTT CAGCGCCTCA GCCCTGGACT GTTAGAGGTG CTGCAGCTGC TCCTGCTCTC 1440
TGATCTTATT GCTTATAAAC TTTGGTGACG GTAGTGTGTA AGGCCGTATT TTTAGCATCT 1500
GACAGGTGTT TACAAAAAAG TGGTTGTCGC ACTGGGAAGT GGAGTGATGG CCTCGTCTCC 1560
AGTGCTCCTC TGGGCTCTTG AGTTGCTGCT TGAATTGCCG TGTAGACATT TGCTTGAGAGA 1620
GTCCACTTGT TATTTGACGG AGGTAGGTTT CAACCCAGAG TTAATGTCAA GCATGCTAAT 1680
TTAACTAGTC ACTCACAGAT GACTTTTCTT TAATAAAGTC CCTTTTCCTA TTAACAAAAA 1740
AA 1742

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1074 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SKINBIT01
- (B) CLONE: 1871375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116 :

GCGGTGCAGA GGAAGCACAA CCTCTACCGG GACAGCATGG TCATGCACAA CAGCGACCCC 60
AACCTGCACC TGCTGGCCGA GGGCGCCCCC ATCGACTGGG GCGAGGAGTA CAGCAACAGC 120
GGCGGGGGCG GCAGCCCAGC CCCAGCACCC CGGAGTCAGC CACCCTCTCG GAAAAGCGAC 180
GGCGCGCCAA GCAGGTGGTC TCTGTGGTCC AGGATGAGGA GGTGGGGCTG CCCTTTGAGG 240
CTAGCCCTGA GTCACCACCA CTGCGTCCC CGGACGGTGT CACTGAGATC CGAGGCCTGC 300
TGGCCCAAGG TCTGCGGCCT GAGAGCCCCC CACCAGCCGG CCCCCTGCTC AACGGGGCCC 360
CCGCTGGGGA GAGTCCCCAG CCTAAGGCCG CCCCCGAGGC CTCCTCGCCG CCTGCCTCAC 420
CCCTCCAGCA TCTCCTGCCT GGAAAGGCTG TGGACCTTGG GCCCCCAAG CCCAGCGACC 480
AGGAGACTGG AGAGCAGGTG TCCAGCCCCA GCAGCCACCC CGCCCTCCAC ACCACCACCG 540
AGGACNANTT TCAAGGGGTG CAAGAATTGA AGNTTCNTAA GGGCCAANTT GGGGGTCCCC 600
TTGACTTGGN TTGNAANAT TGGGGCAAAA AGGGCCGGTT TTCCCNTTT CCCGGGANAC 660
CCCAAGGGAA AGGGGNTTCA AAGCTTCTTN GGGGGGGAAA GGGGGAANCC CTTGGGTNTT 720

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TTGTTGGCCN TTTGTGANCA NCAGCGAGGA GAGTGCAAAG GTGCAGAGTN AGTTNTAGGN 780
CANTGGGTCC CTGACTGCTG CANATGGTAA GGNCGTNNC TTGTGGACCC AAGGCAGGNA 840
AAGNTGTGGG GAGGGAAGCT GGTNTGTGCN TTGTGGGTGG AAGCGGGGAN GGCTGTGTTG 900
NANGGCAGGG AGAGGGCNAA NTGAGTTATT TATTGGGGTT CANGTGAAAA GTTTCTTGNN 960
CCCTGTNTTG TGTNCTGTG GGATTGATTN TAAGATNGNN AGGGGTNGGT TTTTGGGGTT 1020
TTCCTGGTTG GTGGCCAAAN GGGTTGGAAA ATNGNTGGGG GGGGNTTGGA NAAT 1074

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LEUKNOT03
- (B) CLONE: 1880830

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117 :

CCCCGGGGGAG GCCTGACCCC CTCCGCACCA CCGTACGGAG CCGCATTTCC CCCGTTTCCC 60
GAGGGGCATC CAGCCGTGTT GCCTGGGGAG GACCCACCCC CCTATTCACC CTTAACTAGC 120
CCGGACAGTG GGAGTGCCCC TATGATCACC TGCCGAGTCT GCCAATCTCT CATCAACGTG 180
GAAGGCAAGA TGCATCAGCA TGTAGTCAAA TGTGGTGTCT GCAATGAAGC CACCCCAATC 240
AAGAATGCAC CCCCAGGGAA AAAATATGTT CGATGCCCCCT GTAAGTGTCT CCTTATCTGC 300
AAAGTGACAT CCAACGGAT TGCATGCCCT CGGCCCTACT GCAAAAGAAT CATCAACCTG 360
GGGCCTGTGC ATCCCGGACC TCTGAGTCCA GAACCCCAAC CCATGGGTGT CAGGGTTATC 420
TGTGGACATT GCAAGAATAC TTTTCTGTGG ACAGAGTTCA CAGACCGCAC TTTGGCACGT 480
TGTCCCTACT GCAGGAAAGT GTCATCTATT GGGCGCAGAT ACCCACGTAA GAGATGTATC 540
TGCTGCTTCT TGCTTGGCTT GCTTTTGGCA GTCAGTCCA CTGGCCTTGC CTTTGGCACA 600
TGGAAGCATG CACGGCGATA TGGAGGCATC TATGCAGCCT GGGCATTGT CATCCTGTTG 660
GCTGTGCTGT GTTTGGGCCG GGCTCTTTAT TGGGCCTGTA TGAAGGTCAG CCACCCTGTC 720
CAGAACTTCT CCTGAGCCTG ATGACCCACA GACTGTGCCT GGCCCTCCC TGGTGGGGAC 780
AGTGACACTA CGAAGGGAGC TGGGGTAGTT AAAGGCTCCC GGGGCTTCTA GAAGGAAGCC 840
AAGCAGCTGC CTTCTTTTC CCTGGGGAGA GGTAGGAAGG AACCAGGCCC TCACTTAGGT 900
TTGGAGGGGC AGATAAGAGC ACTGCTGACC ATCTGCTTTC CTCCAAGGGT TGCTGTGTCT 960

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AGGGTGAAGT AGGCAAAACG TTGCCCTTAA AACTGGGCCC TGAAGACGGT TCCAGCCTTG 1020
TCCTTCCTGT GTGCTCCCTG AGAGCCATTC CTGTCCCTTA CACATTCCAG GGCAGGGTGG 1080
GGGTGGGTAG CCCTGGGGGT TCCCCTCCCT CTTGTGCACC ATTAGGACTT TGCTGCTGCT 1140
ATTGCACTTC ACCAGAGGTT GGCTCTGGCC TCAGTACCCT CAGTCTCCTC TCCCCACATT 1200
GTGTCCTGTG GGGGTGGGGT CAGCCGCTGC TCTGTACAGA ACCACAGGAA CTGATGTGTA 1260
TATAACTATT TAATGTGGGA TATGTTCCCC TATTCCTGTA TTTCCCTTAA TTCCTCCTCC 1320
CGACCTTTTT TACCCCCCA GTTGCAGTAT TTAAGTGGGC TGGGTAGGGT TGCTCAGTCT 1380
TTGGGGGAGG TTAGGGACTT ATCCTGTGCT GTAAATAAA TAAGGTCATG ACTCTAAAAA 1440
AAAAAAAAGG GCGG 1454

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2071 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: OVARNOT07
- (B) CLONE: 1905325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118 :

AGCTTTGAAT TCCTGTATCT GAGAACGGAT CGTTCGAGGT GGTGGAGGGG GTTGAATTG 60
GGGACCTACG GAAGGCTCAG CTCTTGCCAG GCCAAATTGA GACATGTCTG ACACAAGCGA 120
GAGTGGTGCA GGTCTAACTC GCTTCCAGGC TGAAGCTTCA GAAAAGGACA GTAGCTCGAT 180
GATGCAGACT CTGTTGACAG TGACCCAGAA TGTGGAGGTC CCAGAGACAC CGAAGGCCTC 240
AAAGGCACTG GAGGTCTCAG AGGATGTGAA GGTCTCAAAA GCCTCTGGGG TCTCAAAGGC 300
CACAGAGGTC TCAAAGACCC CAGAGGCTCG GGAGGCACCT GCCACCCAGG CCTCGTCTAC 360
TACTCAGCTG ACTGATACCC AGGTTCTGGC AGCTGAAAAC AAGAGTCTAG CAGCTGACAC 420
CAAGAAACAG AATGCTGACC CGCAGGCTGT GACAATGCCT GCCACTGAGA CCAAAAAGGT 480
CAGCCATGTG GCTGATACAA AGGTCAATAC AAAGGCTCAG GAGACTGAGG CTGCACCCTC 540
TCAGGCCCCA GCAGATGAAC CTGAGCCTGA GAGTGCAGCT GCCCAGTCTC AGGAGAATCA 600
GGATACTCGG CCAAGGTCA AAGCCAAGAA AGCCCGAAAG GTGAAGCATC TGGATGGGGA 660
AGAGGATGGC AGCAGTGATC AGAGTCAGGC TTCTGGAACC ACAGGTGGCC GAAGGGTCTC 720
AAAGGCTCTA ATGGCCTCAA TGGCCCGCAG GTTCAAGGG GTCCCATAGC CTTTTGGGCC 780

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CGCAGGATTC AAGGACTCGG TTGGCTGCTT GGGCCCGGAG AGCCTTGCTC TCCCTGAGAT 840
CACCTAAAGC CCGTAGGGCA AGGCTCGCCG TAGAGCTGCC AAGCTCCAGT CATCCCAAGA 900
GCCTGAAGCA CCACCACCTC GGGATGTGGC CCTTTTGCAA GGGAGGGCAA ATGATTTGGT 960
GAAGTACCTT TTGGCTAAAG ACCAGACGAA GATTCCCATC AAGCGCTCGG ACATGCTGAA 1020
GGACATCATC AAAGAATACA CTGATGTGTA CCCCAGAAATC ATTGAACGAG CAGGCTATTC 1080
CTTGAGAGAAG GTATTTGGGA TTCAATTGAA GGAAATTGAT AAGAATGACC ACTTGATACAT 1140
TCTTCTCAGC ACCTTAGAGC CCACTGATGC AGGCATACTG GGAACGACTA AGGACTCACC 1200
CAAGCTGGGT CTGCTCATGG TGCTTCTTAG CATCATCTTC ATGAATGGAA ATCGGTCCAG 1260
TGAGGCTGTC ATCTGGGAGG TGCTGCGCAA GTTGGGGCTG CGCCCTGGGA TACATCATTC 1320
ACTCTTTGGG GACGTGAAGA AGCTCATCAC TGATGAGTTT GTGAAGCAGA AGTACCTGGA 1380
CTATGCCAGA GTCCCCAATA GCAATCCCCC TGAATATGAG TTCTTCTGGG GCCTGCGCTC 1440
TTACTATGAG ACCAGCAAGA TGAAAGTCCT CAAGTTTGCC TGCAAGGTAC AAAAGAAGGA 1500
TCCCAAGGAA TGGGCAGCTC AGTACCGAGA GGCGATGGAA GCAGATTTGA AGGCTGCAGC 1560
TGAGGCTGCA GCTGAAGCCA AGGCTAGGGC CGAGATTAGA GCTCGAATGG GCATTGGGCT 1620
CGGCTCGGAG AATGCTGCCG GGCCCTGCAA CTGGGACGAA GCTGATATCG GACCCTGGGC 1680
CAAAGCCCGG ATCCAGGCGG GAGCAGAAGC TAAAGCCAAA GCCCAAGAGA GTGGCAGTGC 1740
CAGCACTGGT GCCAGTACCA GTACCAATAA CAGTGCCAGT GCCAGTGCCA GCACCAGTGG 1800
TGGCTTCAGT GCTGGTGCCA GCCTGACCGC CACTCTCACA TTTGGGCTCT TCGCTGGCCT 1860
TGGTGGAGCT GGTGCCAGCA CCAGTGGCAG CTCTGGTGCC TGTGGTTTCT CCTACAAGTG 1920
AGATTTTGA TATTGTTAAT CCTGCCAGTC TTTCTCTTCA AGCCAGGGTG CATCCTCAGA 1980
AACCTACTCA ACACAGCACT CTAGGCAGCC ACTATCAATC AATTGAAGTT GACACTCTGC 2040
ATTAAATCTA TTTGCCATTT CAAAAAAAAA A 2071

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1236 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTTUT01
- (B) CLONE: 1919931

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119 :

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ACCTGGGACC CCCAGAACGG CCGCCCCTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT 60
TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTAG AAGGTTGAAA CCAGGCTTAT 120
TTATTTTCAT CTTCTTTCTG CCATCTTTTA ACCAACCTTC TCAGAATAAA ATGTGATTTT 180
TGAGACAGAA TGAAACACAT ATCCAAATTT TAATACAGTA AGAATAGGTA TCCTGAATAA 240
ATGAGAACTC TAGAAAATCA AGGTTTCAAA ATTCTACCCT TCCTGGGAGT TAAAGAAGTT 300
TGGCAGAAAC AGAACAAATT AATCAGCAGA TTCATCACCT GCCAATTTTT TCTGTACAAT 360
TTTCTTGATT CTGGGAGCAT CTGGGTCCAG GCAGATTTTC CTCCCATCCT TCAGTGTGGC 420
TGCTTCTTGT TTCATCCATG GACCCTGCAA GAAATTGCCC CATGTTTCTG TTTGTGCATC 480
ACTGAGAAAG GAAGCATGAA GGTCGCACAG GTCAGGCCAT TCCATTGCCC TCCTGGTGCC 540
GGGTTTGCCC TCCCAATCCT GGGGTTGCTT CAGGGGCTTG TCATTCTCCA TAGTCCCCTC 600
CACATTTCTC AGGTTTCTGC TCAAAAGTCA CCTTTTGGAG GGGTCTCCAC CTGTCACTGT 660
GTTTGTAAGA GCTCCTTCAG TTTCTTTCTA GCTCATCTCA CTCTGGTAAT GTCTTTGATT 720
ACCACCACCA TCTGACCTGG TCTTATGACC TGTTAGCTTT CTTCATCAGA CGTGAGCACC 780
AGGATGGCAG GGGCCTCATC TGTCTGTTC CTCCTGTGGC CTGGGTCCTA GCACCATGTC 840
TGGTACAGTG TAGATGCTCA AGGGAAGTTT ACTTTGTAAA ACCACTTACC TGGGAGATGT 900
TACTGTTAGT CTAACCTGTA CCATTTTGTA AACCTCCAGC CATTTTGCAG ACTCTGATCA 960
CAGTGAAACG TTCCATGGGA ACTTGGGCCA TGAGAAACAT CCTTCCTAAC CACGTGACTG 1020
CAGAAACATC CTTATCGCGT CCTCCTGGGC AAAGGCCCAA CAGCCTGACT GCAGGGACAT 1080
CCTTGCCATA TCCTGCTGGG CAGCAAGCTC TACCACCCAG ATCCCTCCCT CCCAGTCCCA 1140
TGATTACCCC AGCCTGTGAG TGGCAGTTGG TGCTGGCACT AAGCTGGTTT CCTCCTCCCC 1200
AGGGTTTTCG TGGCAATAAA GATGTTGCTG TTGAAG 1236

(2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTNOT04
- (B) CLONE: 1969426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120 :

GTACTGCCCA CCACCTCCCT GGGCCACCCC TCACTCAGTG CTCGGGCTCT CTCCTCCTCC 60

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TCTTCGTCCT CCTCCACTTC ATCTCCTGTT TTGGGCTCCC CCTCTTACCC TGCTTCTTCC 120
CCTGGGGCCT CCCCCACCA CCGCCGTGTG CCCCTCAGCC CCCTGAGTTT GCTCGCGGGC 180
CCAGCCGACG CCAGAAGGTC CCAACAGCAG CTGCCCCAAC AGTTTTCGCC AACAAATGTCA 240
CCCACCTTGT CTTCCATCAC TCAGGGGCGTC CCCCTGGATA CCAGTAAACT GTCCACTGAC 300
CAGCGGTTAC CCCCATACCC ATACAGCTCC CCAAGTCTGG TTCTGCCTAC CCAGCCCCAC 360
ACCCCAAAGT CTCTACAGCA GCCAGGGCTG CCCTCTCAGT CTTGTTCAGT GCAGTCCTCA 420
GGTGGGCAGC CCCCAGGCAG GCAGTCTCAT TATGGGACAC CGTACCCACC TGGGCCCAGT 480
GGGCATGGGC AACAGTCTTA CCACCGGCCA ATGAGTGACT TCAACCTGGG GAATCTGGAG 540
CAGTTCAGCA TGGAGAGCCC ATCAGCCAGC CTGGTGCTGG ATCCCCCTGG CTTTTCTGAA 600
GGCCTGGAT TTTTAGGGGG TGAGGGGCCA ATGGGTGGCC CCCAGGATCC CCACACCTTC 660
AACCACCAGA ACTTGACCCA CTGTTCCCGC CATGGCTCAG GGCCTAACAT CATCCTCACA 720
GGGGACTCCT CTCCAGGTTT CTCTAAGGAG ATTGCAGCAG CCCTGGCCGG AGTGCCTGGC 780
TTTGAGGTGT CAGCAGCTGG ATTGGAGCTA GGGCTTGGGC TAGAAGATGA GCTGCGCATG 840
GAGCCACTGG GCCTGGAAGG GCTAAACATG CTGAGTGACC CCTGTGCCCT GCTGCCTGAT 900
CCTGCTGTGG AGGAGTCATT CCGCAGTGAC CGGCTCCAAT GAGGGCACCT CATCACCATC 960
CCTCTTCTTG GCCCCATCCC CCACCACCAT TCCTTTCCTC CCTTCCCCCT GGCAGGTAGA 1020
GACTCTACTC TCTGTCCCCA GATCCTCTTT CTAGCATGAA TGAAGGATGC CAAGAATGAG 1080
AAAAAGCAAG GGGTTTGTCC AGGTGGCCCC TGAATTCTGC GCAAGGGATG GGCCTGGGGG 1140
AACTCAAGGG AGGGCCTAAA GCACTTGTA CTTTGAACCG TCTGTCTGGA GGTCAGAGCC 1200
TGTTGGAAAG CAGGGGTAGA GGGGAGCCCT GGAAGCAGGG CTTTTCGGA TGCCTAGGGG 1260
TGGGCAGTGC CAGCCCCTCC TCACCACTCT TCCCCTTGCA GTGGAGGAGA GAGCCAGAGT 1320
GGATACTATT TTTTATTAAA TATATTATTA TATGTTAATA AAAAAATCAT ATCAAAAAAA 1380
AAAAAAAAG G 1391

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: UCMCL5T01
- (B) CLONE: 1969948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121 :

CTCTGTGAAC ATATGATGAG AGAAGCCAAG ATCATGCAGT ATAAGTACCT ACTGTTTCAGT 60
 CTTACACGCCA TAGTGAAGCT TGGAATCCCT CAGAACACTA TTTTGGTGCA GACTTTGCTG 120
 AGGGTGACCC AGGAACGTAT CAATGAGTGT GATGAGATAT GCCTTTCAGT TTTGTCAACT 180
 GTTTTAGAGG CAATGGAACC ATGCAAGAAT GTTCATGTTC TACGAACGGG ATTCAGAATA 240
 CTAGTTGATC AGCAAGTTTG GAAATAGAA GATGTCTTCA CATTACAAGT TGTGATGAAG 300
 TGTATTGGAA AAGATGCACC GATTGCTCTT AAGAGGAAAC TGGAGATGAA AGCCTTGAGG 360
 GGATTAGACA GATTTTCTGT TTTGAATAGC CAACACATGT TTGAAGTACT AGCTGCCATG 420
 AATCACCGAT CTCTTATACT CCTGGATGAA TGCAGTAAGG TGGTCCTAGA TAATATCCAT 480
 GGGTGTCCCTT TAAGAATAAT GATCAACATA TTGCAGTCCT GCAAAGACCT CCAGTACCAT 540
 AATTTGGATC TCTTCAAGGG ACTTGCAGAT TATGTGGCTG CAACTTTCGA CATCTGGAAG 600
 TTCAGAAAAG TTCTTTTTTAT CCTCATTTTA TTTGAAAACC TTGGCTTTCG ACCTGTTGGT 660
 TTAATGGACC TGTTTATGAA GAGAATAGTA GAGGATCCTG AATCCCTAAA CATGAAAAAC 720
 ATTCTATCTA TTCTTCATAC TTA CTCTTCT CTCAATCATG TCTACAAATG CCAGAACAAA 780
 GAACAGTTCG TGGAAGTTAT GGCTAGTGCT CTGACTGGTT ATCTTCACAC TATTTCTTCT 840
 GAAAACTTAT TGGATGCAGT ATATTCATTT TGCTTGATGA ATTACTTTCC CCTGGCTCCT 900
 TTTAATCAGC TTCTGCAAAA AGACATCATC AGTGAGCTGC TGACATCAGA TGACATGAAG 960
 AATGCTTACA AGCTGCATAC TTTGGATACT TGTCTAAAAC TTGATGATAC TGTCTATCTG 1020
 AGGGACATAG CCTTGTCACCT CCCACAGCTG CCGCGGGAGC TGCCATCGTC ACATACAAAT 1080
 GCAAAGGTGG CAGAGGTGCT GAGCAGCCTT CTGGGAGGTG AAGGACACTT CTCAAAGGAT 1140
 GTGCACTTGC CACACAATTA TCATATTGAT TTTGAAATCA GAATGGACAC TAACAGGAAT 1200
 CAAGTGCTAC CACTTTCTGA TGTGGATACA ACTTCTGCTA CAGATATTCA AAGAGTAGCT 1260
 GTGCTATGTG TTTCCAGATC TGCTTATTGT TTGGGTTCAA GCCACCCAG AGGATTCCTT 1320
 GCTATGAAAA TGCGGCATTT GAATGCAATG GGTTTTCATG TGATCTTGGT CAATAACTGG 1380
 GAGATGGACA AACTAGAGAT GGAAGATGCA GTCACATTTT TGAAGACTAA AATCTATTCA 1440
 GTAGAAGCTC TTCCTGTTGC TGCTGTAAAT GTGCAAAGCA CACAATAAAG TGAAAATCAA 1500
 CCTTTTCATA TTAGGAGACA TGCATTTGTA AAAATTAATA AAGATGACAA GTCAGTTGTC 1560
 AATGGAATTG AGCTATCTGC TAAGACAAAA AATGTTACCT CAGTTCAC TAATAATTAA 1620
 TTTTAGGAGT GGAAGAAATG TTGTTACTGC CATTTAAAAA TATGCTGAGA AAATTCCAGA 1680
 AGGGTTATTT TTCCAACCAC ACCTATTCCC TCTAGTGCCC AGATATTTGA TTTGTGAGCT 1740
 GTACGTTTCA CCTTTTCATC TTTGATCTAC TAAAACTGG TTTCTTAGTT GTGAGGTGTC 1800

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ACAGGCAGGT TGATGTGGGT AGTAGTCCTT GTCTTTGGAA TCTGAATATT TATACTCCTG 1860
CTCTAAGCTG TTCTAAGACT TGGGGTTATG CCTTTAAATC ATTTTCAAGC ATTGGCCAAA 1920
TAATAATTGG ACAAAGTTCT AAAGTTGTCA AGTGTGTAAG AATTAGTGAG GTAGCTGTTG 1980
AAAATGAGTG AGGATGGTAT TTGTATTTGT AATAAGCACT GCAGGTAGAG ATATTTTCATG 2040
GGTTATAATA AGAGAAACAC AGATGAGATG TAGATGGTAA GGAGTCTTAC TGTTGTTGGG 2100
GTCCTTCCTT TCTCTTTCTT TTTTCCCCCT TACCCCTCCC ACAATTTTCAT GAAGTCTTTT 2160
AAATTAAATA TATAGCTTNA ATT 2183

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2066 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGAST01
- (B) CLONE: 1988911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122 :

AGAACCACTG CAGTGGAGAC TCCATGTGCA AAAGAAAAAA ACCAAATGTG AGGTCATAAA 60
GACTTTCTGC CAGCATGTGG GTGACATTGT TTCTTTGCAG ATTTTGGCTA TGGAAAGGGG 120
AAATGTTCTA AGCAGAGCCC CGTCAAGAGC CCACGGGACA CATTTTGGAG ATGACAGATT 180
TGAAGATCTG GAAGAGGCAA ATCCATTCTC TTTTAGAGAG TTTCTGAAGA CCAAGAACCT 240
CGGCCTCTCG AAAGAGGATC CGGCCAGCAG AATTTATGCA AAGGAAGCCT CGAGGCATTC 300
CCTGGGACTT GACCACAACT CCCCACCCTC CCAAACCGGC GGGTATGGCC TGGAGTATCA 360
GCAGCCATTT TTCGAGGATC CGACAGGGGC TGGTGACCTC CTGGATGAGG AGGAGGATGA 420
GGACACCGGA TGGAGTGGGG CCTACCTGCC GTCCGCCATC GAGCAGACTC ACCCCGAGAG 480
GGTCCCTGCC GGCACGTCGC CCTGCAGCAC ATACCTTTCC TTTTCTCCA CCCCCTCGGA 540
GCTGGCAGGG CCTGAGTCTC TGCCCTCGTG GGCGTTGAGT GACACTGATT CTCGCGTGTC 600
TCCGGCCTCT CCGGCAGGGA GTCCTAGCGC AGACTTTGCG GTTCATGGAG AGTCTCTGGG 660
AGACAGGCAC CTGCGGACGC TGCAGATAAG TTACGACGCA CTGAAAGATG AAAATTCTAA 720
GCTGAGAAGA AAGCTGAATG AGGTTTCAGAG CTTCTCTGAA GCTCAAACAG AAATGGTGAG 780
GACGCTTGAG CGGAAGTTAG AAGCAAAAAT GATCAAGGAG GAAAGCGACT ACCACGACCT 840
GGAGTCGGTG GTTCAGCAGG TGGAGCAGAA CCTGGAGCTG ATGACCAAAC GGGCTGTAAA 900

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GGCAGAAAAC CACGTCGTGA AACTAAAACA GGAAATCAGT TTGCTCCAGG CGCAGGTCTC 960
CAACTTCCAG CGAGAGAATG AAGCCCTGCG GTGCGGCCAG GGTGCCAGCC TGACCGTGGT 1020
GAAGCAGAAC GCCGACGTGG CCCTGCAGAA CCTCCGGGTG GTCATGAACA GTGCACAGGC 1080
TTCCATCAAG CAACTGGTTT CCGGAGCTGA GACACTGAAT CTTGTTGCCG AAATCCTTAA 1140
ATCTATAGAC AGAATTTCTG AAGTTAAAGA CGAGGAGGAA GACTCTTGAG GACCCCTGGG 1200
TGTTCTCAGC ATGAAGCTCC GTGTATACCC TGAGGTCACC ACCGCTCGAT CTAAATGTGC 1260
AGTTGTGTCC TTAAATATGC AGTCTTCACC CAGAGTAAAG TGTGATCGC AAGAGTCCAG 1320
TGTCGTGCCC TCAGCCAGTT CTTGGCCACC ACAATGGGAG CAGCCCTGGC CGAGTTGTCT 1380
CTGTGGTTTC TATGCAGCCC TTCTTGCGCA AATTCCTGCG ATCTTATAGA TTCTAATGAG 1440
CTCTTGGAAG ACATTGTCAT AAAAGCCAGT GATTTTAAGA AAAAGAGTGG TTCTGGAATC 1500
AATGTTTTCC AGTCCCATCC CAGAACATCA GTTGTAAGAT AAGTACAATT GGTTGTCCTT 1560
GATTTTCATAA GTAGAACAAA CACTAAATGT GCCTCTGAGA TGGCCACCCC GGGCAGGGAC 1620
CTGTGCCTTC CGCCGATGCT CAGGGCTCCC TCTGGCTCCC GGGTCACTCT TGTGGCCCCA 1680
GTGGGTGGTC CCTGCAGTCA TGGCCTGAGT GCGCAGGGGC CACCGCGTGG CTGCTGCTGT 1740
CCTCCTCCGG GACCCACGGG GACCAAGGTC ACACGTCCG TGCTGTGAAG CTGTCCAGAT 1800
GTGCCTCTTT GGCTGGGGGT TCTGGTGGAC GTTTC AAGTG GCATTTTGTA CAATGCAGGT 1860
TAGAATTCAG GAATTTCAAG TATGTGCCCG GGTCTGTCAG GTCCAGTTG CCTTTCTGAC 1920
GGCCCCCTC AGAGGGACGG CGATGAGCAC TAAATGCTTT TTTGACTATT TTCCTATAGA 1980
TTTTTTTTTAA AACTTTTTTT TCCTCCTGTT CCAATTGATA GCTTTCTTAT TTAATAAATT 2040
CTGTAGTTCA CCGCAAAAAA AAAAAA 2066

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1867 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: OVARNOT03
- (B) CLONE: 2061561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123 :

TGGCCAGGCT GGTCTAGAAC TCCTGACTGC AAATGATCAG CCCGCCTCAG CCACCCAAAG 60
TGTGTTGGGATT ACAGGTGTGA GCCACTGTGC CCAGCGTGAT TTTTTTTTTT TTAAAGCAA 120

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ACTTGTCCCTT TGGTTTTGCA GAACAGGCCT GCTCCCTCTC ATCTAGCCCA TCATTTCTTG 180
GGGCCTGAAC CCCAGTGGTC CAAAGTATTG CTTGTGAAAT TTAAAAAATG TGAATATGAT 240
GTGGGGATGG GCCTCTTCTA CATTACCTTG GCCCAGGGGG ATCAGCTGGC TGGGAGGATT 300
AGTGAGCACC TCTGTATTTT GAGGTCTGAG TCTTCTGGAG CTGTGTAGTT AATCTTCGGT 360
TTCTGATAAC CCCTGGGTCC ATCTGGCCAT CAGCCTCAGC AGTGAGCAAA GCAATACCAT 420
ACTCATTTCT ATGTTCCCTGT TCCTTCCTCT GCTCCTCCTT TGGAGAAGCA ATAATTCATG 480
GGGGATGATA CAGTAGCACT TTACAAATGG CTCCATGTCA TTCATCCCAG GGGCCATAAT 540
CTCTTGACACC ACCTATTCTT ACTTCCTGTT CAGCTCCTTT ACAGCTTTTA TTTTCAACTG 600
CTTCCCAACT TGGTGGGGCC TCCTTTAAGG ATGAGCCAAT AGTAAGAATG TGGCTGTAAT 660
CAGCAGAGAC CCCTCTGAGG GGTATCTGTT CTGCAGCCCC TAGTGAAATC ATGTGATGTG 720
AGACAGAAAC CTAAACATGG TACTTGATTC TAAACCTGTG CCAGTCTATA GCCTCTGCCT 780
CCCCAAGCAG AGCTCAAGCC AAACGCTTCT GTCTCTTTTC CTTCTGCATT AACCCTTTGC 840
TGATCCTCAG GGGCCACTCC CCCAACACCC CTGTACTTGG GTGAGGGATG TTGGACAGAG 900
CCTGTTTTCA TGTA CTGAG GTGGGGGTGT GCTGACATGT TTGCTCTTGG TTGATGGAGA 960
AGGTACAGAG GCCAGGGAGT GAAAATGGTT GACAGAAGAG GGAAGAGTTA GGTGTCTCAT 1020
AGTCACTCAT AGTGGGGTGG TCAGGGGTAA TGGCATCTCC CCACTTTAGG CTTCTCAAAC 1080
AGACTTTTGA CACCTCTCAA GTTCAGAGCT CTGATGTGGA AAGACAGGAG GTGTGGGGAA 1140
GGAGGGGGAT TTCGTGTGTT TGCATGAGTG TGCGCTTCAG GCCTTGGGAG TTGGCAAGAG 1200
GGAGGGAAGG AAGGAGAGCA AAATCTTCGG AAGGTGTTTC TTGTACCTGA GGGATCCTGC 1260
CCTGAATCTC CATAGTCTCC ACTGTGAACT GAGGAGGGGA GGGGTGTGCT GGGGAATAAA 1320
TCTTGTATGA GAACAATCAA AAATCAAACG AATCCCACCG ACAGACTGCT GCTCCTAGTG 1380
ATCTGGACTC ACCTAGGGGG CATCTGGGCT GGGGTTCAN GCTTACGTNC GCGTGNATGN 1440
GACGNCANAG CTCTTCGAAA GTGTCCCNAA ANTNC AATTC ATTGGCGGTG GTTTTAAAAG 1500
TTCGGGCCTG GGAAACCCGG GGGNTTACCC ATTTTATCCC NCTTNGANGG CANATTCCCC 1560
TTTTTCCCCA ATTTGGGGAA ATTTNCCAAA NGGNNCCCGT AACGGTTGGC CTTTTCCCAA 1620
AATTTNGGNC GCCCTTAATT GGGGCGATTG TGGGACCCGC GCCCTTTATA GGGGGGGGCT 1680
TTAAAGCGGC GCNNGGGGTT CTTTGGGTGA TTACCGGCGC GGTTGACCCC GGGTAAAATA 1740
TTGACAAGGG CCCTTTAGCG CGCGGTTCTT TGTGGGGTTT TCCTCCCAT TGTCTTTTCC 1800
GCAAAAGTTT TGGCGGGGTT TTCCCCGGAA AAGGTCTTAA AAAGCGGTGT GCCCCTCTTT 1860
GAGGGGG 1867

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1628 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PANCNOT04
- (B) CLONE: 2084489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124 :

CTCTGGGTCT GTAGCAACCG CCCAGCGTTG AGGCGCGGCT CATGCCCCCA GTATCCCGGT 60
 CCAGCTATTC CGAGGACATC GTGGGCTCTC GGAGAAGGCG ACGCAGCTCC TCGGGGAGCC 120
 CACCATCCCC GCAGAGCAGA TGTTCTCTTT GGGATGGCTG TTCCCGCTCT CACTCCCGCG 180
 GCCGTGAGGG CCTCAGGCCT CTTTGGAGTG AGTTGGACGT GGGCGCTCTT TACCCCTTTA 240
 GTCGCTCTGG GTCGCGAGGG CGGCTCCCAA GATTCCGCAA CTACGCCTTC GCGTCCTCCT 300
 GGTGACCTC GTATAGTGA TATCGCTACC ATCGTCACTG CTATGCAGAA GAACGGCAGT 360
 CAGCGGAAGA CTACGAGAAG GAAGAGAGCC ATCGGCAGAG GAGGCTGAAG GAGAGAGAGA 420
 GGATTGGGGA ATTGGGAGCG CCTGAAGTGT GGGGGCCGTC TCCAAAGTTC CCTCAGCTAG 480
 ATTCTGACGA ACATACCCCA GTTGAGGATG AAGAAGAGGT AACGCATCAG AAAAGCAGCA 540
 GTTCAGATTC CAACTCGGAA GAACATAGGA AAAAGAAGAC CAGTCGTTCA AGAAACAAGA 600
 AAAAAAGAAA GAATAAGTCG TCTAAAAGAA AGCATAGGAA ATATTCTGAT AGTGACAGTA 660
 ACTCAGAGTC TGACACAAAT TCTGACTCTG ATGATGATAA AAAGAGAGTT AAAGCCAAGA 720
 AGAAAAAGAA GAAAAAGAAA CACAAAACAA AGAAAAAGAA GAATAAGAAA ACCAAAAAAG 780
 AATCCAGTGA CTCAAGCTGT AAAGACTCAG AAGAGGACTT GTCAGAAGCT ACCTGGATGG 840
 AGCAGCCAAA TGTGGCAGAT ACTATGGATT TAATAGGGCC AGAAGCACCT ATAATACATA 900
 CCTCTCAAGA TGAAAAACCT TTGAAGTATG GCCATGCTTT GCTTCCCGGT GAAGGTGCAG 960
 CTATGGCTGA GTATGTAAAA GCTGGAAAGC GAATCCCACG AAGAGGTGAA ATTGGGTTGA 1020
 CAAGTGAAGA GATCGGTTCT TTTGAATGCT CAGGTTATGT CATGAGTGGT AGCAGGCATC 1080
 GCAGAAATGA GGCTGTACGA CTGCGTAAGG AGAACCAGAT CTACAGTGCT GATGAGAAGA 1140
 GAGCTCTTGC ATCCTTTAAC CAAGAAGAGA GACGAAAGAG AGAAAGTAAG ATTTTAGCCA 1200
 GTTCCGAGA GATGGTGCAC AAAAAGACAA AAGAGAAAGA TGACAAGTAA GGACTTACTT 1260
 GTTGCACAGC AGGAATTTTA ACAACAAAAA TTTTATGTGA CCAAAAGTGT TAAAAGGCTT 1320
 TACAGTGCTA CTGTACTTAC CATATTAGTA AGTCCCTCAG GAAAAAGCTT CTTTTGAGAT 1380

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ATCTTTAGCA GCTTATTTTT TGTTATTTTA ACTTTAAAAA GTAATATGTG CACATGGTTT 1440
TAAAAATATT CAACCATTAT AGGAGGAGAG TTAGTAAAAA GTGAATCTTT CACTTTAGCC 1500
CCTGACACCT TTCCCCCAA AATATATATT TTGGTGTCTT ATATACAGAA TATACATTCT 1560
GTGCATATAC AAGAGTATAT GTTGCAGCAT AAAGATTAAA AGCTATTAAA GTTTTTTTTC 1620
GCTCGTTA 1628

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SPLNFET02
- (B) CLONE: 2203226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125 :

GTGGCGGCGG CGAAGGATGC ACCCGGCAGG CTTGGCGGCG GCGGCTGCGG GGACGCCCCG 60
GCTGCCCTCG AAGCGGAGGA TCCCTGTGTC CCAGCCGGGC ATGGCCGACC CCCACCAGCT 120
TTTCGATGAC ACAAGTTCAG CCCAGAGCCG GGGCTATGGG GCCCAGCGGG CACCTGGTGG 180
CCTGAGTTAT CCTGCAGCCT CTCCCACGCC CCATGCAGCC TTCCTGGCTG ACCCGGTGTC 240
CAACATGGCC ATGGCCTATG GGAGCAGCCT GGCCGCGCAG GGCAAGGAGC TGGTGGATAA 300
GAACATCGAC CGCTTCATCC CCATCACCAA GCTCAAGTAT TACTTTGCTG TGGACACCAT 360
GTATGTGGGC AGAAAGCTGG GCCTGCTGTT CTTCCCCTAC CTACACCAGG ACTGGGAAGT 420
GCAGTACCAA CAGGACACCC CGGTGGCCCC CCGCTTTGAC GTCAATGCCC CGGACCTCTA 480
CATTCCAGCA ATGGCTTTCA TCACCTACGT TTTGGTGGCT GGTCTTGCGC TGGGGACCCA 540
GGATAGGTTT TCCCCAGACC TCCTGGGGCT GCAAGCGAGC TCAGCCCTGG CCTGGCTGAC 600
CCTGGAGGTG CTGGCCATCC TGCTCAGCCT CTATCTGGTC ACTGTCAACA CCGACCTCAC 660
CACCATCGAC CTGGTGGCCT TCTTGGGCTA CAAATATGTC GGGATGATTG GCGGGGTCCT 720
CATGGGCCTG CTCTTCGGA AGATTGGCTA CTACCTGGTG CTGGGCTGGT GCTGCGTGGC 780
CATCTTTGTG TTCATGATCC GGACGCTGCG GCTGAAGATC TTGGCAGACG CAGCAGCTGA 840
GGGGGTCCCG GTGCGTGGGG CCCGGAACCA GCTGCGCATG TACCTGACCA TGGCGGTGGC 900
GGCGGCGCAG CCTATGCTCA TGTA CTGGCT CACCTTCCAC CTGGTGCGGT GAGCGCGCCC 960
GCTGAACCTC CCGCTGCTGC TGCTGCTGCT GGGGGCCACT GTGGCCGCCG AACTCATCTC 1020

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CTGCCTGCAG GCCCAAGGT CCACCCTGTC TGGCCACAGG CACCGCCTCC ATCCCATGTC 1080
CCGCCCAGCC CCGCCCCCAA CCAAGGTGC TGAGAGATCT CCAGCTGCAC AGGCCACCGC 1140
CCCAGGGCGT GGCCGCTGTT ACAGAAACAA TAAACCCTGA TGGGCATGGC AAAAAAAAAA 1200

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1093 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNOT16
- (B) CLONE: 2232884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126 :

AGAGCCCCAG CCACGCCGGC CCAGGTGGCC TCAGGTGAGG GGGGGCGGAC GCACCTGTGG 60
GGACGGGACG ACGAGTTCAA GCCTCCGTGG GTGCAGTTGG TCGCCAGCGA GGGATGCGGA 120
GACGCCCCTG AACGACCATG GCATCGGCCG ACGAGCTGAC CTTCCATGAA TTCGAGGAGG 180
CCACTAATCT TCTGGCTGAC ACCCCAGATG CAGCCACCAC CAGCAGAAGC GATCAGCTGA 240
CCCCACAAGG GCACGTGGCT GTGGCCGTGG GCTCAGGTGG CAGCTATGGA GCCGAGGATG 300
AGGTGGAGGA GGAGAGTGAC AAGGCCGCGC TCCTGCAGGA GCAGCAGCAG CAGCAGCAGC 360
CGGGATTCTG GACCTTCAGC TACTATCAGA GCTTCTTTGA CGTGGACACC TCACAGGTCC 420
TGGACCGGAT CAAAGGCTCA CTGCTGCCCC GGCCTGGCCA CAACTTTGTG CGGCACCATC 480
TGCGGAATCG GCCGGATCTG TATGGCCCCC TCTGGATCTG TGCCACGTTG GCCTTTGTCC 540
TGGCCGTCAC TGGCAACCTG ACGCTGGTGC TGGCCCAGAG GAGGGACCCC TCCATCCACT 600
ACAGCCCCCA GTTCCACAAG GTGACCGTGG CAGGCATCAG CATCTACTGC TATGCGTGGC 660
TGGTGCCCCC GGCCCTGTGG GGCTTCCTGC GGTGGCGCAA GGGTGTCCAG GAGCGCATGG 720
GGCCCTACAC CTTCTTGGAG ACTGTGTGCA TCTACGGCTA CTCCCTCTTT GTCTTCATCC 780
CCATGGTGGT CCTGTGGCTC ATCCCTGTGC CTTGGCTGCA GTGGCTCTTT GGGGCGCTGG 840
CCCTGGGCCT GTCAGCCGCC GGGCTGGTAT TCACCCCTCTG GCCCGTGGTC CGTGAGGACA 900
CCAGGCTGGT GGCCACAGTG CTGCTGTCCG TGGTCGTGCT GCTCCACGCC CTCCTGGCCA 960
TGGGCTGTAA GTTGTACTTC TTCCAGTCGC TGCCTCCGGA GAACGTGGCT CCTCCACCCC 1020
AAATCACATC TCTGCCCTCA AACATCGCGC TGTCCCCTAC CTTGCCGCAG TCCCTGGCCC 1080
CCTCCTAGGA AGG 1093

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNNOT11
- (B) CLONE: 2328134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127 :

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GCGGGGGGATG ACGCCACGGA CATGGTGGCC GAGACCGGCG GGGTGGGGGA CGTGTCGCGC 60
GGCCGGGTGG CCTCGGTCGG TACCCTGGGC GCGGACAGCT GCCTCATTAG TATTCGTACC 120
CACGAGGCGG CGCAGCGGGC CCTCGGGGAC AGCGAGCGTC GCGGCTATGG CTTATCACTC 180
GGGCTACGGA GCCCACGGCT CCAAGCACAG GGCCCGGGCA GCCCGGATC CCCCTCCCT 240
CTTCGATGAC ACAAGCGGTG GTTATTCCAG CCAGCCCGGG GGATACCCAG CCACAGGAGC 300
AGACGTGGCC TTCAGTGTCA ACCACTTGCT TGGGGACCCA ATGGCCAATG TGGCTATGGC 360
CTATGGCAGC TCCATCGCAT CCCATGGGAA GGACATGGTG CACAAGGAGC TGCACCGTTT 420
TGTGTCTGTG AGCAAACCTCA AGTATTTTTT TGCTGTGGAC ACAGCCTACG TGGCCAAGAA 480
GCTAGGGCTG CTGGTCTTCC CCTACACACA CCAGAACTGG GAAGTGCAGT ACAGTCGTGA 540
TGCTCCTCTG CCCCCCGGC AAGACCTCAA CGCCCCTGAC CTCTATATCC CCACGATGGC 600
CTTCATTACT TACGTGCTCC TGGCTGGGAT GGCACCTGGC ATTCAGAAAA GGTTCTCCCC 660
GGAGGTGCTG GGCCTGTGTG CAAGCACAGC GCTGGTGTGG GTGGTGATGG AGGTGCTGGC 720
CCTGCTCCTG GGCCTCTACC TGGCCACCGT GCGCAGTGAC CTGAGCACCT TTCACCTGCT 780
GGCCTACAGT GGCTACAAAT ACGTGGGAAT GATCCTCAGT GTGCTCACGG GGCTGCTGTT 840
CGGCAGCGAT GGCTACTACG TGGCGCTGGC CTGGACCTCA TCGGCGCTCA TGTACTTCAT 900
TGTGCGCTCT TTGCGGACAG CAGCCCTGGG CCCCACAGC ATGGGGGGCC CCGTCCCCCG 960
GCAGCGTCTC CAGCTCTACC TGACTCTGGG AGCTGCAGCC TTCCAGCCCC TCATCATATA 1020
CTGGCTGACT TTCCACCTGG TCCGGTGACC CCCTGGCCCC AGATGGCACT GAGTTTTTCA 1080
TTCATTGAAG ATTTGATTTC CTTGAAAAAA AAAAAAAAAG G 1121

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(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1861 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: ISLTNOT01
 (B) CLONE: 2382718

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128 :

CGCGGACTGT GTCTGTTCCC AGGAGTCCTT CGGCGGCTGT TGTGTCAGTG GCCTGATCGC 60
 GATGGGGACA AAGGCGCAAG TCGAGAGGAA ACTGTTGTGC CTCTTCATAT TGGCGATCCT 120
 GTTGTGCTCC CTGGCATTGG GCAGTGTTAC AGTGCACTCT TCTGAACCTG AAGTCAGAAT 180
 TCCTGAGAAT AATCCTGTGA AGTTGTCCTG TGCCTACTCG GGCTTTTCTT CTCCCCGTGT 240
 GGAGTGGAAG TTTGACCAAG GAGACACCAC CAGACTCGTT TGCTATAATA ACAAGATCAC 300
 AGCTTCCTAT GAGGACCGGG TGACCTTCTT GCCAACTGGT ATCACCTTCA AGTCCGTGAC 360
 ACGGGAAGAC ACTGGGACAT ACACTTGTAT GGTCTCTGAG GAAGGCGGCA ACAGCTATGG 420
 GGAGGTCAAG GTCAAGCTCA TCGTGCTTGT GCCTCCATCC AAGCCTACAG TTAACATCCC 480
 CTCCTCTGCC ACCATTGGGA ACCGGGCAGT GCTGACATGC TCAGAACAAG ATGGTTCCCC 540
 ACCTTCTGAA TACACCTGGT TCAAAGATGG GATAGTGATG CCTACGAATC CAAAAGCAC 600
 CCGTGCCTTC AGCAACTCTT CCTATGTCCT GAATCCCACA ACAGGAGAGC TGGTCTTTGA 660
 TCCCCTGTCA GCCTCTGATA CTGGAGAATA CAGCTGTGAG GCACGGAATG GGTATGGGAC 720
 ACCCATGACT TCAAATGCTG TGCGCATGGA AGCTGTGGAG CGGAATGTGG GGGTCATCGT 780
 GGCAGCCGTC CTTGTAACCC TGATTCTCCT GGAATCTTG GTTTTGGCA TCTGGTTTGC 840
 CTATAGCCGA GGCCACTTTG ACAGAACAAA GAAAGGGACT TCGAGTAAGA AGGTGATTTA 900
 CAGCCAGCCT AGTGCCCGAA GTGAAGGAGA ATTCAAACAG ACCTCGTCAT TCCTGGTGTG 960
 AGCCTGGTCG GCTCACCGCC TATCATCTGC ATTTGCCTTA CTCAGGTGCT ACCGGACTCT 1020
 GGCCCTGAT GTCTGTAGTT TCACAGGATG CCTTATTTGT CTTCTACACC CCACAGGGCC 1080
 CCCTACTTCT TCGGATGTGT TTTTAATAAT GTCAGCTATG TGCCCCATCC TCCTTCATGC 1140
 CCTCCCTCCC TTTCTACCA CTGCTGAGTG GCCTGGAAGT TGTTTAAAGT GTTTATTCCC 1200
 CATTTCTTTG AGGGATCAGG AAGGAATCCT GGGTATGCCA TTGACTTCCC TTCTAAGTAG 1260
 ACAGCAAAAA TGGCGGGGGT CGCAGGAATC TGCACTCAAC TGCCACCTG GCTGGCAGGG 1320
 ATCTTTGAAT AGGTATCTTG AGCTTGGTTC TGGGCTCTTT CTTGTGTAC TGACGACCAG 1380
 GGCCAGCTGT TCTAGAGCGG GAATTAGAGG CTAGAGCGGC TGAAATGGTT GTTTGGTGAT 1440
 GAACTGGGG TCCTTCCATC TCTGGGGCCC ACTCTCTTCT GTCTTCCCAT GGAAGTGCC 1500

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ACTGGGATCC CTCTGCCCTG TCCTCCTGAA TACAAGCTGA CTGACATTGA CTGTGTCTGT 1560
GGAAAATGGG AGCTCTTGTT GTGGAGAGCA TAGTAAATTT TCAGAGAACT TGAAGCCAAA 1620
AGGATTTAAA ACCGCTGCTC TAAAGAAAAG AAAACTGGAG GCTGGGCGCA GTGGCTCACG 1680
CCTATAATCC CAGAGGCTGA GGCAGGCGGA TCACCTGAGG TCGGGAGTTC GGGATCAGCC 1740
TGACCAACAT GGAGAAACCC TACTGAGAAT ACAAAGTTAG CCAGGCATGG TGGTGCATGC 1800
CTGTAATCCC AGCTGCTCAG GAGCCTGGCA ACAAGAGCAA AACTCCAGCT CAAAAAAAAA 1860
A 1861

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1975 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: ENDANOT01
- (B) CLONE: 2452208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129 :

GTTTGGAGGA GACTCGGATA TACCTTCTCA GAAGCTGCAC AGGAGGAAAG CAGTGACAAA 60
GAAAGAAGTT GTCATTCTTT GCACGAAACT GGATGGCTTC TACAGGGAGC CAGGCCTCTG 120
ATATAGACGA GATTTTTGGA TTCTTCAACG ATGGCGAACC TCCCACCAA AAGCCCAGGA 180
AGCTGCTTCC AAGCTTAAAA ACTAAGAAGC CTCGAGAACT TGTGCTAGTG ATTGGAACAG 240
GCATTAGTGC TGCAGTTGCG CCCCAAGTTC CAGCCCTCAA ATCCTGGAAG GGGTTAATTC 300
AGGCCTTACT GGATGCTGCC ATTGATTTTG ATCTTTTAGA AGATGAGGAG AGCAAAAAGT 360
TTCAGAAATG TCTCCATGAA GACAAGAACC TGGTCCATGT TGCCCATGAC CTTATCCAGA 420
AACTCTCTCC TCGTACCAGT AATGTTTCGAT CCACATTTTT CAAGGACTGT TTATATGAAG 480
TATTTGATGA CTTGGAGTCA AAGATGGAAG ATTCTGGAAA ACAGCTACTT CAGTCAGTTC 540
TCCACCTGAT GGAAAATGGA GCCCTCGTAT TAACTACAAA TTTTGATAAT CTCTTGGAAC 600
TGTATGCAGC AGATCAGGGG AAACAGCTTG AATCCCTTGA CTTACTGAT GAGAAAAAGG 660
TCCTCGAGTG GGCTCAGGAG AAGCGTAAGC TGAGCGTGTT GCATATTCAC GGAGTCTACA 720
CCAACCCTAG TGGCATTGTC CTTCATCCGG CTGGATATCA GAACGTGCTC AGGAACACTG 780
AAGTCATGAG AGAAATTGAG AAACCTCTACG AAAACAAGTC ATTTCTTTTC CTGGGCTGTG 840
GCTGGACTGT GGATGACACC ACTTTCCAGG CCCTTTTCTT GGAGGCTGTC AAGCATAAAT 900

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CTGACCTAGA ACATTTTCATG CTGGTTTCGGA GAGGAGACGT AGATGAGTTC AAAAAGCTTC 960
GAGAAAACAT GCTGGACAAG GGGATTAAAG TCATCTCCTA TGGAGATGAC TATGCCGATC 1020
TTCCAGAATA TTTCAAGCGA CTGACATGTG AGATCTCCAC AAGGGGTACA TCAGCAGGGA 1080
TGGTGAGAGA AGGTCAGCTA AATGGCTCAT CTGCAGCACA CAGTGAAATA AGAGGCTGTA 1140
GTACATGAGC GAGCTAGAGA AATCACCACC GTTTAGACCA AGCTGTAAGG CCCTACTACA 1200
GACAGTGTTC AACAAAGTAAA CTTACAAGAA CCCAACACAA TTCCCAGAAA GTAACAATAG 1260
CCAGAGGTTG AAGGGCGGGG TAGAAGAGGG GGAATGTTG CAGCGTAATC CTTCATACCA 1320
CCTGGTTCTT GATATTCTGC CGCCTGTTCA AGTTCAAGAA TAAAAGCGAC AGCAGGACCC 1380
AAATGCAGCT CCCAACCCAC TCCCCAGGCT AGACATGCTT GTGTCCACAC AGCACACCAA 1440
TGTGATACTT CCACTGACCG GCTGCAGCTC TGCATGAAGG ACTCGGGGTC TGGATGCCAT 1500
GGAATCACTG TGGCTCTTGT TGCAGTTTTG TACTCTATAC TTGGTTTTTC AATTAAGCTT 1560
AATGGCTTTT TTTAAACATG ACTTGAAGCT CTAGTTTTCT AGATCTTTTA CAGTGTACAG 1620
TATTTTACAT AACTAAGCTG TATTAAAAGC TTGTTCAATTT ACTTGCCAGG ACCCTGGCTC 1680
TACTTTTAGA GTCATTGTAA GAAACTCTAA CTTGCATCAA GGTACTAATA AGCTTAATTT 1740
TAATAACCCA AAGTTTAAAG GTTCCGATCT TTCTCCTTGG GGTGGAGTGA TCTCATTCTC 1800
AGGACAACCG TTTACTTACC TGATTCCTCG GAGCATTATC AACTTCTGCT CTGTTGTCCT 1860
GACCATACAT ATGTCCTAGA ACTACAGTTA AGTGTGTTGT GGAATTTTAG TTTTGAATCC 1920
GGAATAAATG AAGTCCCAGG ACTCAAAGAA GAGAGAAAAA AAAAAAGGGG GCCCC. 1975

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: ENDANOT01
- (B) CLONE: 2457825

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130 :

TCTACTGTCC CCTGCCCTGT ACCCCCAGGC ATTGATCTGG AGAACATTGT GTECTACAAG 60
GACGACACCC ACTACTTTGT GATGACAGCC AAGAAGCAGT GCCTGCTGCG GCTGGGGGTG 120
CTGCGCCAGG ACTGGCCAGA CACCAATCGG CTGCTGGGCA GTGCCAATGT GGTGCCCCGAG 180
GCTCTGCAGC GCTTTACCCG GGCAGCTGCT GACTTTGCCA CCCATGGCAA GCTCGGGAAA 240

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CTAGAGTTTG CCCAGGATGC CCATGGGCAG CCTGATGTCT CTGCCTTTGA CTTACGAGC 300
ATGATGCGGG CAGAGAGTTC TGCTCGTGTG CAAGAGAAGC ATGGCGCCCG CCTGCTGCTG 360
GGACTGGTGG GGGACTGCCT GGTGGAGCCC TTCTGGCCCC TGGGCACTGG AGTGGCACGG 420
GGCTTCCTGG CAGCCTTTGA TGCAGCCTGG ATGGTGAAGC GGTGGGCAGA GGGCGCTGAG 480
TCCCTAGAGG TGTTGGCTGA GCGTGAGAGC CTGTACCAGC TTCTGTCACA GACATCCCCA 540
GAAAACATGC ATCGCAATGT GGCCAGTAT GGGCTGGACC CAGCCACCCG CTACCCCAAC 600
CTGAACCTCC GGGCAGTGAC CCCCAATCAG GTACGAGACC TGTATGATGT GCTAGCCAAG 660
GAGCCTGTGC AGAGGGACAA CGACAAGACA GATACAGGGA TGCCAGCCAC CGGGTCGGCA 720
GGCACCCAGG AGGAGCTGCT ACGCTGGTGC CAGGAGCAGA CAGCTGGGTA CCCGGGAGTC 780
CACGTCTCCG ATTTGTCTTC CTCCTGGGCT GATGGGCTAG CTCTGTGTGC CCTGGTGTAC 840
CGGCTGCAGC CTGGCCTGCT GGAACCCCTCA GAGCTGCAGG GGCTGGGAGC TCTGGAAGCA 900
ACTGCTTGGG CACTAAAGGT GGCAGAGAAT GAGCTGGGCA TCACACCGGT GGTGTCTGCA 960
CAGGCCGTGG TAGCAGGGAG TGACCCACTG GGCCTCATTG CCTACCTCAG CCACTTCCAC 1020
AGTGCCTTCA AGAGCATGGC CCACAGCCCA GGCCCTGTCA GCCAGGCCTC CCCAGGGACC 1080
TCCAGTGCTG TATTATTCCT TAGTAAACTT CAGAGGACCC TGCAGCGATC CCGGGCCAAG 1140
GAAAATGCAG AGGATGCTGG TGGCAAGAAG CTGCGCTTGG AGATGGAGGC CGAGACCCCA 1200
AGTACTGAGG TGCCACCTGA CCCAGAGCCT GGTGTACCCC TGACACCCCA ATCCCAACAC 1260
CAGGAGGCCG GTGCTGGGGA CCTGTGTGCA CTTTGTGGGG AACACCTCTA TGTCTGGAA 1320
CGCCTCTGTG TCAACGGCCA TTTCTTCCAC CGGAGCTGCT TCCGCTGCCA TACCTGTGAG 1380
GCCACACTGT GGCCAGGTGG CTACGAGCAG CACCCAGGCA GTAGAACGTC TCAGTTCTTC 1440
TTCTCAGCTC TTGTGGCCAT GGAGAAGGAG GAAAAAGAGA GTCCCTTCTC CAGTGAAGAG 1500
GAAGAAGAAG ATGTGCCTTT GGA CTAGAT GTGGAACAGG CCCTGCAGAC CTTTGCCAAG 1560
ACCTCAGGCA CCATGAATAA CTACCCAACA TGGCGTCGGA CTCTGCTGCG CCGTGCGAAG 1620
GAGGAGGAGA TGAAGAGGTT CTGCAAGGCC CAGACCATCC AACGGCGACT AAATGAGATT 1680
GAGGCTGCCT TGAGGGAGCT AGAGGCCGAG GGCCTGAAGC TGGAGCTGGC CTTGAGGCGC 1740
CAGAGCAGTT CCCCAGAACA GCAAAAGAAA CTATGGGTAG GACAGCTGCT ACAGCTCGTT 1800
GACAAGAAAA ACAGCCTGGT GGCTGAGGAG GCCGAGCTCA TGATCACGGT GCAGGAATTG 1860
AATCTGGAGG AGAAACAGTG GCAGCTGGAC CAGGAGCTAC GAGGCTACAT GAACCGGGAA 1920
GAAAACCTAA AGACAGCTGC TGATCGGCAG GCTGAGGACC AGGTCCTGAG GAAGCTGGTG 1980
GATTTGGTCA ACCAGAGAGA TGCCCTCATC CGCTTCCAGG AGGAGCGCAG GCTCAGCGAG 2040
CTGGCCTTGG GGACAGGGGC CCAGGGCTAG ACGAGGGTGG GCCGTCTGCT TTCGTTCCCA 2100

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CAAAGAAAGC ACCTCACCCC AGCACAGTGC CACCCCTGTT CATCTGGGCT GCCTGGCAGA 2160

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THP1NOT03
- (B) CLONE: 2470740

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131 :

GAGGAAGAAG AGGAAGAGGG GGCTCCGATT GGGACCCCTA GGGATCCTGG AGATGGTTGT 60
CCTTCCCCCG ACATCCCTCC TGAACCCCT CCAACACACC TGAGGCCCTG CCCTGCCAGC 120
CAGCTCCCTG GACTCCTGTC CCATGGCCTC CTGGCCGGCC TCTCCTTTGC AGTGGGGTCC 180
TCCTCTGGCC TCCTGCCCCT CCTGCTGCTG CTGCTGCTTC CATTGCTGGC AGCCCAGGGT 240
GGGGGTGGCC TGCAGGCAGC GCTGCTGGCC CTTGAGGTGG GGCTGGTGGG TCTGGGGGCC 300
TCCTACCTGC TCCTTTGTAC AGCCCTGCAC CTGCCCTCCA GTCTTTTCCT ACTCCTGGCC 360
CAGGGTACCG CACTGGGGGC CGTCCTGGGN CATGAGCTGG CGCCGAAGGC TCATGGGTGT 420
TCCCCTGGGG CTTTGGAACT GCCTGGTTCT TAAGCTTNGG CAAGGCCTAG CTCCAACCTC 480
TGGTGGCTAA TGGCANCCGG GGGGGAANAT GGGTTCNGGA AAAAGGGCCC CCGGGTTTCA 540
CCGGGG 546

(2) INFORMATION FOR SEQ ID NO: 132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SMCANOT01
- (B) CLONE: 2479092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132 :

GCCATGGAGG CCCTGAGGAG GGCCACGAG GTCGCGCTCC GCCTGCTGCT GTGTAGGCCG 60
TGGGCCTCGC GCGCCGCCGC CCGCCCCAAG CCCAGCGCCT CGGAGGTGCT GACGCGGCAT 120

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CTGCTGCAGC GGCGCCTGCC GCACTGGACC TCCTTCTGCG TGCCCTACAG CGCCGTCCGC 180
AACGACCAGT TCGGCCTCTC GCACTTCAAC TGGCCGGTGC AGGGCGCCAA CTACCACGTC 240
CTGCGCACCG GCTGCTTCCC CTTTCATCAAG TACCACTGCT CCAAGGCTCC CTGGCAGGAC 300
CTGGCCCGGC AGAACCGCTT CTTACGGCG CTCAAGGTCG TCAACCTCGG TATTCCAAC 360
TTATTATATG GACTTGGCTC CTGGTTATTT GCCAGAGTCA CAGAGACTGT GCATACCAGT 420
TATGGACCCA TAACAGTTTA TTTTCTCAAT AAAGAAGATG AAGGTGCCAT GTATTGAAAG 480
TGTGCGTCAA AGAACATAAA TATCAGTGGA TTTTCTCTGT GTATATGTGC AGTATTTATT 540
TTTGATCCTT TAAAATAAAA CTTTTGCAA TAAAAAAAAA A 581

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1259 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SMCANOT01
- (B) CLONE: 2480544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133 :

GGGCTGGGCC CCGCCGAGC TCCAGCTGGC CGGCTTGGTC CTGCGGTCCC TTCTCTGGGA 60
GGCCCGACCC CGGCCGCGCC CAGCCCCAC CATGCCACCC GCGGGGCTCC GCCGGGCCGC 120
GCCGCTCACC GCAATCGCTC TGTTGGTGCT GGGGGCTCCC CTGGTGCTGG CCGGCGAGGA 180
CTGCCTGTGG TACCTGGACC GGAATGGCTC CTGGCATCCG GGGTTTAACT GCGAGTTCTT 240
CACCTTCTGC TGCGGGACCT GCTACCATCG GTACTGCTGC AGGGACCTGA CCTTGCTTAT 300
CACCGAGAGG CAGCAGAAGC ACTGCCTGGC CTTAGCCCC AAGACCATAG CAGGCATCGC 360
CTCAGCTGTG ATCCTCTTTG TTGCTGTGGT TGCCACCACC ATCTGCTGCT TCCTCTGTTC 420
CTGTTGCTAC CTGTACCGCC GGCGCCAGCA GCTCCAGAGC CCATTTGAAG GCCAGGAGAT 480
TCCAATGACA GGCATCCCAG TGCAGCCAGT ATACCCATAC CCCCAGGACC CCAAAGCTGG 540
CCCTGCACCC CCACAGCCTG GCTTCATGTA CCCACCTAGT GGTCTGCTC CCCAATATCC 600
ACTCTACCCA GCTGGGCCCC CAGTCTACAA CCCTGCAGCT CCTCCTCCCT ATATGCCACC 660
ACAGCCCTCT TACCCGGGAG CCTGAGGAAC CAGCCATGTC TCTGCTGCCC CTTAGTGAT 720
GCCAACCTTG GGAGATGCCC TCATCCTGTA CCTGCATCTG GTCCTGGGGG TGGCAGGAGT 780
CCTCCAGCCA CCAGGCCCCA GACCAAGCCA AGCCCTGGGC CCTACTGGGG ACAGAGCCCC 840

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AGGGAAGTGG AACAGGAGCT GAACTAGAAC TATGAGGGGT TGGGGGGAGG GCTTGAATT 900
ATGGGCTATT TTTACTGGGG GCAAGGGAGG GAGATGACAG CCTGGGTCAC AGTGCCTGTT 960
TTCAAATAGT CCCTCTGCTC CCAAGATCCC AGCCAGGAAG GCTGGGGCCC TACTGTTTGT 1020
CCCCCTCTGGG CTGGGGTGGG GGGAGGGAGG AGGTTCCGTC AGCAGCTGGC AGTAGCCCTC 1080
CTCTCTGGCT GCCCCACTGG CCACATCTCT GGCCTGCTAG ATTAAAGCTG TAAAGACATA 1140
ACTCATATCA GTCGCATCAT TGGACCCATC CACACCTTCC AGGAACACCG NCTTCAGCTG 1200
GGCCCAGACT GTTGCCCACT CCATATTCCA AAAGTAGGGG AGGGCCAGCA CCAGCATCG 1259

(2) INFORMATION FOR SEQ ID NO: 134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2033 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAITUT21
- (B) CLONE: 2518547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134 :

CGGCTCGAGG CCGCAGCCCC ATGGACAGTC TTCTGCACCC CCGGGAGCGC CCTGGATCCA 60
CTGCCTCCGA GAGCTCAGCC TCTCTGGGCA GTGAGTGGA CCTCTCAGAA TCTTCTCTCA 120
GCAACCTGAG TCTTCGCCGT TCCTCAGAGC GCCTCAGTGA CCCCCCTGGA TCCTTCCAGT 180
CACCTTCCCT GGAAATTCTG CTGTCCAGCT GCTCCCTGTG CCGTGCCTGT GATTGCTGG 240
TGTATGATGA GGAAATCATG GCTGGCTGGG CACCTGATGA CTCTAACCTC AACACAACCT 300
GCCCCCTCTG CGCCTGCCCC TTTGTGCCCC TGCTCAGTGT CCAGACCCTT GATTCCCGGC 360
CCAGTGTCCT CAGCCCCAAA TCTGCTGGTG CCAGTGGCAG CAAAGATGCT CCTGTCCCTG 420
GTGGTCCTGG CCCTGTGCTC AGTGACCGAA GGCTCTGCCT TGCTCTGGAT GAGCCCAGCT 480
CTGCAACGGG CACATGGGGG GAGCCTCCCG GCGGGTTGAG AGTGGGGCAT GGGCATACT 540
GAGCCCCCTG GTGCTGCGTA AGGAGCTGGA GTCGCTGGTA GAGAACGAGG GCAGTGAGGT 600
GCTGGCGTTG CCTGAACTGC CCTCTGCCCA CCCCATCATC TTCTGGAACC TTTTGTGGTA 660
TTTCCAACGG CTACGCCTGC CCAGTATTCT ACCAGGCCTG GTGCTGGCCT CCTGTGATGG 720
GCCTTCGCAC TCCCAGGCCC CATCTCCTTG GCTAACCCTT GATCCAGCCT CTGTTCAGGT 780
ACGGCTGCTG TGGGATGTAC TGACCCTGA CCCCAATAGC TGCCCACCTC TCTATGTGCT 840
CTGGAGGGTC CACAGCCAGA TCCCCAGCG GGTGGTATGG CCAGGCCCTG TACCTGCATC 900

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CCTTAGTTTG GCACTGTTGG AGTCAGTGCT GCGCCATGTT GGACTCAATG AAGTGCACAA 960
GGCTGTGGGG CTCCTGCTGG AAACCTCTAGG GCCCCACCC ACTGGCCTGC ACCTGCAGAG 1020
GGGAATCTAC CGTGAGATAT TATTCCTGAC AATGGCTGCT CTGGGCAAGG ACCACGTGGA 1080
CATAGTGGCC TTCGATAAGA AGTACAAGTC TGCCTTTAAC AAGCTGGCCA GCAGCATGGG 1140
CAAGGAGGAG CTGAGGCACC GCGGGGCGCA GATGCCCACT CCAAGGCCA TTGACTGCCG 1200
AAAATGTTTT GGAGCACCTC CAGAATGCTA GAGACCTTAA GCTTCCCTCT CCAGCCTAGG 1260
GTGGGGAAGT GAGGAAGAAG GGATTCTAGA GTTAAACTGC CTCCCTGTTG CCTTCATGGA 1320
GTTGGGAACA GGCTGGGAAG GATGCCCAGT CAAAGGCTCC AAGCGAGGAC AACAGGAAGA 1380
GGGATCCACT GTTACCAAAA GTCCTGATTC CCCCATCACC AACCTACCCA GTTTGTTCTG 1440
GCTGATGTTG GGGGAGATCT GGGGGGAGTT GGTACAGCTC TGTTCCTCCC TTGTCCTATA 1500
CCGGGAACTC CCCTCCAGGG TACCCACAGA TCTGCATTGC CCTGGTCATT TTAGAAGTTT 1560
TTGTTTTTAA AAACAACCTG AAAGATGCAG AGCTACTGAG CCTTTGCCCT GAATGGGAGG 1620
TAGGGATGTC ATTCTCCACC AATAATGGTC CCTCTTCCCT GACGTTGCTG AAGGAGCCCA 1680
AGGCTCTCCA TGCCTTTCTA CCTAAGTGTT TGTATTTTAT TTTAAATTAT TTATTCTGGA 1740
GCCACAGCCC CCTTGCTTAT GAGGTTCTTA TGGAGAGTGA GAAAGGGAAG GGAAATAGGG 1800
CACCATGGTC CGGTGGTTTG TAGTTCCTTC AAAGTCAGGC ACTGGGAGCT AGAGGAGTCT 1860
CAAGCTCCCC TTAGGAAGAA CTGGTGCCCC CTCCAGTCCT AATTTTCTT GCCTGCCCCG 1920
CCTTGGGGAA TGCCTCACCC ACCCAGGTCC TGACCTGTGC AATAAGGATT GTTCCCTGCG 1980
AAGTTTTGTT GGATGTAAAT ATAGTAAAAG CTGCTTCTGT CTTTTTCAAA AAA 2033

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3007 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GBLANOT02
- (B) CLONE: 2530650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135 :

GCCCACTGGG CTCTCCCGGC TGCAGTGCCA GGGCGCAGGA CGCGGCCGAT CTCCCGCTCC 60
CGCCACCTCC GCCACCATGC TGCTCCCCCA GCTCTGCTGG CTGCCGCTGC TCGCTGGGCT 120
GCTCCCGCCG GTGCCCCTC AGAAGTTCTC GCGCTCACG TTTTGTGAGAG TGGATCAAGA 180

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TAAAGACAAG GATTGTAGCT TGGACTGTGC GGGTTCGCCC CAGAAACCTC TCTGCGCATC 240
TGACGGAAGG ACCTTCCTTT CCCGTTGTGA ATTTCAACGT GCCAAGTGCA AAGATCCCCA 300
GCTAGAGATT GCATATCGAG GAAACTGCAA AGACGTGTCC AGGTGTGTGG CCGAAAGGAA 360
GTATACCCAG GAGCAAGCCC GGAAGGAGTT TCAGCAAGTG TTCATTCCTG AGTGCAATGA 420
CGACGGCACC TACAGTCAGG TCCAGTGTCA CAGCTACACG GGATACTGCT GGTGCGTCAC 480
GCCCCACGGG AGGCCCATCA GCGGCACTGC CGTGGCCCCAC AAGACGCCCC GGTGCCCGGG 540
TTCCGTAAAT GAAAAGTTAC CCCAACGCGA AGGCACAGGA AAAACAGATG ATGCCGCAGC 600
TCCAGCGTTG GAGACTCAGC CTCAAGGAGA TGAAGAAGAT ATTGCATCAC GTTACCCTAC 660
CCTTTGGACT GAACAGGTTA AAAGTCGGCA GAACAAAACC AATAAGAATT CAGTGTTCATC 720
CTGTGACCAA GAGCACCAGT CTGCCCTGGA GGAAGCCAAG CAGCCCAAGA ACGACAATGT 780
GGTGATCCCT GAGTGTGCGC ACGGCGGCCT CTACAAGCCA GTGCAGTGCC ACCCCTCCAC 840
GGGGTACTGC TGGTGCCTCC TGGTGGACAC GGGGCGCCCC ATTCCCGGCA CATCCACAAG 900
GTACGAGCAG CCGAAATGTG ACAACACGGG CCAGGGCCCCA CCCAGCCAAA GCCCGGGACC 960
TGTACAAGGG CCGCCAGCTA CAAGGTTGTC CGGGTGCCAA AAAGCATGAG TTTCTGACCA 1020
GCGTTCTGGA CGCGCTGTCC ACGGACATGG TCCACGCCGC CTCCGACCCC TCCTCCTCGT 1080
CAGGCAGGCT CTCAGAACCC GACCCAGCC ATACCCTAGA GGAGCGGGTG GTGCACTGGT 1140
ACTTCAAAC ACTGGATAAA AACTCCAGTG GAGACATCGG CAAAAGGAA ATCAAACCCCT 1200
TCAAGAGGTT CCTTCGCAA AAATCAAAGC CCAAAAAATG TGTGAAGAAG TTTGTTGAAT 1260
ACTGTGACGT GAATAATGAC AAATCCATCT CCGTACAAGA ACTGATGGGC TGCCTGGGCG 1320
TGGCGAAAGA GGACGGCAAA GCGGACACCA AGAAACGCCA CACCCCCAGA GGTCATGCTG 1380
AAAGTACGTC TAATAGACAG CCAAGGAAAC AAGGATAAAT GGCTCATACC CCGAAGGCAG 1440
TTCCTAGACA CATGGGAAAT TTCCCTCACC AAAGAGCAAT TAAGAAAACA AAAACAGAAA 1500
CACATAGTAT TTGCACTTTG TACTTTAAAT GTAAATTCAC TTTGTAGAAA TGAGCTATTT 1560
AAACAGACTG TTTTAATCTG TGAAAATGGA GAGCTGGCTT CAGAAAATTA ATCACATACA 1620
ATGTATGTGT CCTCTTTTGA CCTTGGAAT CTGTATGTGG TGGAGAAGTA TTTGAATGCA 1680
TTTAGGCTTA ATTTCTTCGC CTTCCACATG TTAACAGTAG AGCTCTATGC ACTCCGGCTG 1740
CAATCGTATG GCTTTCTCTA ACCCCTGCAG TCACTTCCAG ATGCCTGTGC TTACAGCATT 1800
GTGGAATCAT GTTGAAGCT CCACATGTCC ATGGAAGTTT GTGATGTACG GCCGACCCTA 1860
CAGGCAGTTA ACATGCATGG GCTGGTTTGT TTCTTGGGAT TTTCTGTTAG TTTGTCTTGT 1920
TTTGCTTTCC AGAGATCTTG CTCATACAAT GAATCACGCA ACCACTAAAG CTATCCAGTT 1980
AAGTGCAGGT AGTTCCTCTG GAGGAAATAA TATTTTCAA CTGTCGTTGG TGTGATACTT 2040

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GGGCTCAAAG GATCTTTGCT TTTCCATTTT AAGCTTCTGT TTTGAGTTTT GCCCTGGGGC 2100
TTGAATGAGT CCCAGAGAGT CGTTCGGATG GTGGGAGGCT GCCTAGGAGG CAGTAAATCC 2160
AGTCACAGTG CCTGGGAGGG GCCCATCCTT CCAAAATGTA AATCCAGTCG CGGTGTGACC 2220
GAGCTGGCTA ACAGGCTTGT CTGCCTGGTT TTCCTCCTAC ACGTGGACAT TATTCTCCTG 2280
ATCCTCCTAC CTGGTCCACC CCAGGGCTAC CGGAAGGTAA AATCTTCACC TGAACCAATT 2340
ATGAGCAGTC TCCTTACTGA AGGTACAGCC GGATACGTGG TGCCCCCGGG GCTGGTGTG 2400
GCAGCCGGGG GGAGGTGCCT GAGGGTCCCC ACGGTTCCCTT TCTGCTTTTC TGAATGCATC 2460
AAGGGTACGA GAACTTGCCA ATGGGAAATT CATCCGAGTG GCACTGGCAG AGAAGGATAG 2520
GAGTGGAATG CCCACACAGT GACCAACAGA ACTGGTCTGC GTGCATAACC AGCTGCCACC 2580
CTCAGGCCTG GGCCCCAGAG CTCAGGGCAC CCAGTGTCTT AAGGAACCAT TTGGAGGACA 2640
GTCTGAGAGC AGGAACTTCA AGCTGTGATT CTATCTCGGC TCAGACTTTT GGTTGGAAAA 2700
AGATCTTCAT GGCCCCAAT CCCCTGAGAC ATGCCTTGTA GAATGATTTT GTGATGTTGT 2760
GATGCTTGTG GAGCATCGCG TAAGGCTTCT TGCTTATTTA AACTGTGCAA GGTA AAAATC 2820
AAGCCTTTGG AGCCACAGAA CCAGCTCAAG TACATGCCAA TGTGTTTAA GAAACAGTTA 2880
TGATCCTAAA CTTTTTGGAT AATCTTTTAT ATTTCTGACC TTTGAATTTA ATCATTGTTT 2940
TTAGATTAAA ATAAATATG CTATTGAAAC TAAAAA AAAAGAGGGGA GAAGAAAAA 3000
AAAAAGG 3007

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1229 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THYMNOT04
- (B) CLONE: 2652271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136 :

CTCTCTGCTC CGGTGCAGGC CCGCAGGCGC CCTGGGCTGG GAGCAACGCG ACTGACCGTG 60
GTCGTGGGCG GACGGCGGCT GCAGCGTGGA GGAGCTGGGG TCGCTGTGGG TCGCGAACAG 120
AGCCCCGGGAC GTGCGCGCTT GGTGCACGAT CCTGAAGGGG AGCTCCGAGG GGCCCCGGGTC 180
TCCAGGGCTG CTGCGGCCAT TCCCGGAGCC CGGCGCGGGG CCCGCGAGAT ACTGGTTTAG 240
GCCGTCCCAG GGCTCCGGGC GCACCCGGTG GCCGCTGCTG CAGCGGAGGG AGCGCGGCGG 300

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CGCGGGGGCT CGGAGACAGC GTTCTCTCCG GAAGTCTTCC TCGGGCAGCA GGTGGGAAGT 360
GGGAGCCGGA GCGGCAGCTG GCAGCGTTCT CTCCGCAGGT CGGCACCATG CGCCCTGCAG 420
CCCTGCGCGG GGCCCTGCTG GGCTGCCTCT GCCTGGCGTT GCTTTGCCTG GCGGGTGCAG 480
ACAAGCGCCT GCGTGACAAC CATGAGTGGA AAAAATAAT TATGGTTCAG CACTGGCCTG 540
AGACAGTATG CGAGAAAATT CAAAACGACT GTAGAGACCC TCCGATTAC TGGACAATAC 600
ATGGACTATG GCCCCATAAA AGTGAAGGAT GTAATAGATC GTGGCCCTTC AATTTAGAAG 660
AGATTAAGGA TCTTTTGCCA GAAATGAGGG CATACTGGCC TGACGTAATT CACTCGTTTC 720
CCAATCGCAG CCGCTTCTGG AAGCATGAGT GGGAAAAGCA TGGGACCTGC GCCGCCAGG 780
TGGATGCGCT CAACTCCCAG AAGAAGTACT TTGGCAGAAG CCTGGAAGTC TACAGGGAGC 840
TGGACCTCAA CAGTGTGCTT CTAAAATTGG GGATAAAACC ATCCATCAAT TACTACCAAG 900
TTGCAGATTT TAAAGATGCC CTTGCCAGAG TATATGGAGT GATACCCAAA ATCCAGTGCC 960
TTCCACCAAG CCAGGATGAG GAAGTACAGA CAATTGGTCA GATAGAAGTC TGCCTCACTA 1020
AGCAAGACCA GCAGCTGCAA AACTGCACCG AGCCGGGGGA GCAGCCGTCC CCCAAGCAGG 1080
AAGTCTGGCT GGCAAATGGG GCCGCCGAGA GCCGGGGTCT GAGAGTCTGT GAAGATGGCC 1140
CAGTCTTCTA TCCCCACCT AAAAAGACCA AGCATTGATG CCCAAGTTT GGAAATATTC 1200
TGTTTTAAAA AGCATGAGGT AGGCATGTC 1229

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1972 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGTUT11
- (B) CLONE: 2746976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137 :

ACAGGGGCTT CCCCTTCGCC GCCGCCGCCG CCGCCGGCCA AGCTCCGCCG CGCCCGCGGC 60
CCGCGGCCGC CATGCAGTTT ATGTTGCTTT TTAGTCGTCA GGGAAAGCTT CACTGCAAA 120
AATGGTATGT CCCACTATCA GACAAAGAGA AGAGAAAGAT CACAAGAGAA CTTGTTTCTA 180
CCGTTTTAGC ACGGAAACCT AAAATGTGCA GCTTCCTTGA GTGGCGAGAT CTGAAGATTG 240
TTTACAAAAG ATATGCTAGT CTGTATTTTT GCTGTGCTAT TGAGGATCAG GACAATGAAC 300
TAATTACCCT GGAAATAATT CATCGTTATG TGAATTACT TGACAAGTAT TTCGGCAGTG 360

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TCTGTGAACT AGATATCATC TTTAATTTTG AGAAGGCTTA TTTTATTTTG GATGAGTTTC 420
TTTTGGGAGG GGAAGTTCAG GAAACATCCA AGAAAAATGT CCTTAAAGCA ATTGAGCAGG 480
CTGATCTACT GCAGGAGGAT GCGAAAGAAG CTGAAACCCC ACGTAGTGTT CTTGAAGAAA 540
TTGGACTGAC ATAACTCTCC TCCCTTGTTG ATGACTTCTT GTGGCATTTC ACACACTGTA 600
GATGGTCACT CCCTTCATGT CCATGTTAGC TCATGGTGTA AGATGATGTC TTGTCAGTAT 660
TACTGTTTTG CTAAGCCGCT TCATTCATGC CTACACAATT TTTTTTTAAA AGGGAACTTT 720
AGTTAATTAA GTGATAAGGG ACTTAAATAT GAATTAGAAT GGTGCAGAAA GAGATACCTT 780
TTCTGGATAT TTTAAAGTTT AAAGGTCAGT TTCTCTTAAT CTGATTATGT GCACATATGA 840
AAATGGCACA TCATATACAT GTAAAATCAG GCAGTATACA TTTATTAATT ACTGTATTTG 900
ACAAAGGAAA CTCTTAAATT ATAATGTGAA ACCTGGTTTT ATGAAACCAA AGACTAGTGC 960
AGCATTTTCAG CATATGTAAA AAAAAAAAAA AAGGGAATTG ACATGTCACA TATCAAATGA 1020
ATGGAAACTT TGTGAAACT TTA AAAAGCA AATTTACTCC AAAGACTTGT ATTGGAAATT 1080
ACATACCTTT TTTTTTTTTT TTTAAAGGAC TACAGATTAT TTTAATGAC TAAATTGGAG 1140
TGATACTTCT TACTATAAAA ATTATTTCTT AGGCATTCTG AATCTGGGAT GAGAAACAGG 1200
ATTGTTTCAC AATAGTAAGC ACATAATTTT TAAGGCCAAG GCACATTTGA CTCCTGAGAT 1260
GAATTTTTTG TGGTCATAAT CAAATACTTA GTTGTTTTTG ATGCCCCAAA ATAAAGTGAG 1320
AATGGTAATT TGCCAGGAAT TCTTCATAAC AGTATCTTAC AAAAAACGTG TTGCTCTCTT 1380
CACAGTATTA TGTGTAAAGT CATTGTTTAA AGCACGAATG TTCCCTCTGG GGTACTTGTT 1440
AAAGCTAAAT TTATTTTGCT TCCCTCCACT TAGAAGTGCT GCACACTTTA CAGCAGCTTC 1500
CTTTCTTTCC ATGGCACTGC CTAGTTAACA GAAGTCTTAT AAAAATTTAA AAAGACACAT 1560
TTCTTACAAA AAAGAGTTGA ATGAGGTAAA ATGGCATTAG ATGGCTCTAT ATTTTTTAAA 1620
GCTATGTAAT TGTTCAGCGT CACTTTTCTA AGTACTTATA CATATCTAAA CATGTCTTCA 1680
TGTTTTATAT TTCACTTAT ATATGCTGGG CTGGATTAAG CTTTGTTGTG ATTGTGACCA 1740
ACATTCAGGC CACGTGAGCA CTGTCTTATC ACATCGCCAA TTAGTTGTAA TAAACGTTCA 1800
ACGTACAAAC ACTGGAGTGT GTTTTTATCT CTTTCCAAAA GTTTGTCAAA CTATGCAGAG 1860
CTGCTGAAGG AAGAATTTCT CATTTTTTTT TCAGTAAAT GTTGAAAATT CCCCTCCATT 1920
TGAATATGGT GGTGTGTATA AGCACACACA AGATACATGG TGGAAGATCT AG 1972

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 1741 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: THP1AZS08
(B) CLONE: 2753496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138 :

CGGGTTCCGG GCTCCGGGCT CTGGGTGGCG GCGGCTGTGA GCNGCGGCTG ANCCNCCGCG 60
CTGCGCANCG ACGCGGGAAT GAAGCGGGCG CTGGGCAGGC GAAAGGGCGT GTGGTTGCGC 120
CTGAGGAAGA TACTTTTCTG TGTTTTGGGG TTGTACATTG CCATTCCATT TCTCATCAAA 180
CTATGTCCTG GAATACAGGC CAAACTGATT TTCTTGAATT TCGTAAGAGT TCCCTATTTT 240
ATTGATTTGA AAAAACCACA GGATCAAGGT TTGAATCACA CGTGTAATA CTACCTGCAG 300
CCAGAGGAAG ACGTGACCAT TGGAGTCTGG CACACCGTCC CTGCAGTCTG GTGGAAGAAG 360
GCCCCAAGGCA AAGACCAGAT GTGGTATGAG GATGCCTTGG CTTCCAGCCA CCCTATCATT 420
CTGTACCTGC ATGGGAACGC AGGTACCAGA GGAGGCGACC ACCGCGTGGA GCTTTACAAG 480
GTGCTGAGTT CCCTTGTTA CCATGTGGTC ACCTTTGACT ACAGAGGTTG GGGTGACTCA 540
GTGGGAACGC CATCTGAGCG GGGCATGACC TATGACGCAC TCCACGTTTT TGA CTGGATC 600
AAAGCAAGAA GTGGTGACAA CCCC GTGTAC ATCTGGGGCC ACTCTCTGGG CACTGGCGTG 660
GCGACAAATC TGGTGCGGCG CCTCTGTGAG CGAGAGACGC CTCCAGATGC CCTTATATTG 720
GAATCTCCAT TACTAATAT CCGTGAAGAA GCTAAGAGCC ATCCATTTTC AGTGATATAT 780
CGATACTTCC CTGGGTTTGA CTGGTTCTTC CTTGATCCTA TTACAAGTAG TGGAATTAAA 840
TTTGCAAATG ATGAAAACGT GAAGCACATC TCCTGTCCCC TGCTCATCCT GCACGCTGAG 900
GACGACCCGG TGGTGCCCTT CCAGCTTGGC AGAAAGCTCT ATAGCATCGC CGCACCAGCT 960
CGAAGCTTCC GAGATTTCAA AGTTCAGTTT GTGCCCTTTC ATTCAGACCT TGGCTACAGG 1020
CACAAATACA TTTACAAGAG CCCTGAGCTG CCACGGATAC TGAGGGAATT CCTGGGGAAG 1080
TCGGAGCCTG AGCACCAGCA CTGAGCCTGG CCGTGGGAAG GAAGCATGAA GACCTCTGCC 1140
CTCCTCCCGT TTTCTTCCAG TCAGCAGCCC GGTATCCTGA AGCCCCGGGG GGCCGGCACC 1200
TGCAATGCTC AGGAGCCCAG CTCGCACCTG GAGAGCACCT CAGATCCCAG GTGGGGAGGC 1260
CCCTGCAGGC CTGCAGTGCC CGGAGGCCTG AGCATGGCTG TGTGGAAAGC GTGGGTGGCA 1320
GGCATGTGGC TCTCCTTGCC GCCCTCAAC CTGAGATCTT GTTGGGAGAC TTAATGGCAG 1380
CAGGCAGCCA TACTGCCTG GTTGATGCTG CACTGAGCTG GACAGGGGGA GTCCGGGCAG 1440
GGGACTCTTG GGGCTCGGGA CCATGCTGAG CTTTTTGGCA CCACCCACAG AGAACGTGGG 1500

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GTCCAGGTTC TTTCTGCACC TTCCCAGCAC ATGCAGAATG ACTCCAGTGG TTCCATCGTC 1560
CCCTCCTGCC CTGTGTACCT GCTTGCCTTT CTCAGCTGCC CCACCTCCCC TGGGCTGGCC 1620
CACTCACCCA CAGTGGAACT GCCCGGGATC TGCACTTCCT CCCCTTTCAC CTACCTGTAC 1680
ACCTAACCTG GCCTTAGACT GAGCTTTATT TAAGAATAAA ATCGTGGTGG TGAACAAAAA 1740
A 1741

(2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2808 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: OVARTUT03
- (B) CLONE: 2781553

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139 :

GGCAAGATGG CGGAAGGGGA GGACGTGGGA TGGTGGCGGA GCTGGCTGCA GCAGAGCTAC 60
CAAGCAGTCA AAGAGAAGTC CTCTGAAGCC TTGGAGTTTA TGAAGCGGGA CCTGACGGAG 120
TTTACCCAGG TGGTGCAGCA TGACACGGCC TGTACCATCG CAGCCACGGC CAGCGTGGTC 180
AAGGAGAAGC TGGCTACGGA AGGCTCCTCA GGAGCAACAG AGAAGATGAA GAAAGGGTTA 240
TCTGACTTCC TAGGGGTGAT CTCAGACACC TTTGCCCCCT CGCCAGACAA AACCATCGAC 300
TGCGATGTCA TCACCCTGAT GGGCACACCG TCTGGCACAG CTGAGCCCTA TGATGGCACC 360
AAGGCTCGCC TCTATAGCCT GCAGTCGGAC CCAGCAACCT ACTGTAATGA ACCAGATGGG 420
CCCCCGGAAT TGTTTGACGC CTGGCTTTCC CAGTTCTGCT TGGAGGAGAA GAAGGGGGAG 480
ATCTCAGAGC TCCTTGTAAG CAGCCCCTCC ATCCGGGGCC TCTACACCAA GATGGTTCCA 540
GCAGCTGTTT CCCATTGAGA ATTCTGGCAT CGGTATTTCT ATAAAGTCCA TCAGTTAGAG 600
CAGGAGCAGG CCCGGAGGGA CGCCCTGAAG CAGCGGGCGG AACAGAGCAT CTCTGAAGAG 660
CCCGGCTGGG AGGAGGAGGA AGAGGAGCTC ATGGGCATTT CACCCATATC TCCAAAAGAG 720
GCAAAGGTTC CTGTGGCCAA AATTTCTACA TTCCCTGAAG GAGAACCTGG CCCCAGAGC 780
CCCTGTGAAG AGAATCTGGT GACTTCAGTT GAGCCCCCAG CAGAGGTGAC TCCATCAGAG 840
AGCAGTGAGA GCATCTCCCT CGTGACACAG ATCGCCAACC CGGCCACTGC ACCTGAGGCA 900
CGAGTGCTAC CCAAGGACCT GTCCCAAAAG CTGCTAGAGG CATCCTTGGA GGAACAGGGC 960
CTGGCTGTGG ATGTGGGTGA GACTGGACCC TCACCCCTA TCACTCCAA GCCCCTAACG 1020

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CCTGCTGGCC ACACCGGCGG CCCAGAGCCC AGGCCTCCAG CCAGAGTAGA GACTCTGAGG 1080
GAGGAGGCGC CCACAGACTT ACGGGTGTTT GAGCTGAACT CGGATAGTGG GAAGTCTACA 1140
CCCTCCAACA ATGGAAAGAA AGGCTCAAGC ACGGACATCA GTGAGGACTG GGAGAAAGAC 1200
TTTGA CT TGG ACATGACTGA AGAGGAGGTG CAGATGGCAC TTTCCAAAGT GGATGCCTCC 1260
GGGGAGCTGG AAGATGTAGA GTGGGAGGAC TGGGAGTGAG GGAGCCAGAG GGAGCAGCTC 1320
CCCCACCCAT GGCATCTCTC GCCTCCCTCG CTCGTCTCAG CCCAGCCCTG GAAGACTGAG 1380
AATGTTCCCC CAAATCTCCT CTGCCAACCA GAGCTCTGGG CACAGATTCT GGTGGCTCCC 1440
TGCTGGCCCT CT TGGG CCTC TGCTCACACC TGGGAAGGGG CTCTCTAAAT CCCGGCCAGA 1500
AACTCTGACT TGTGCCAACA ATAGGATGAC CCAAGGGAGA GGAAACCTAT CCTCCTCACC 1560
AGAAGAGCCT GTGTTTTTCT GCTGAACACC CACTGTTCTT GAGGACTCCT GCTGGGAAGT 1620
CCCAAGGGAT AGTTC TAGCC CTTCTGCCTG TG TAGACAGA AGCTAAACCA CCAGTCTCTC 1680
TCGGAGGAAG CTGAGACAAC ATACTCTGTC CATAcataag CAGGCAGGGA GGGCCATGCC 1740
ACCTACCCTT GGCTAAACAG GGACAGTGAA CACATTTTGG TTCCTATCCC AGTGGGTAAG 1800
AGGCACTTAT CTCTGGGAAA TTTGCCTCTC TTGGGACTCT CCCCCTCCA GGCATTTTCC 1860
ATTCTTGAA AGGCTCCTTT GGGGTTT CAGA ATCCAGAGAC CAAACCCTGA CCCACCTCCT 1920
TCCTTTCTC CAGCCCACGC TGGTCTGTCC CCATGCCTTC CCAGGGCTTC TTCATGTCAG 1980
ATGCACCCAA GTCCTTAGCC CAGCTGTGCC ACCTGCAGGA GTTCGCTCTT GCGTTTCTTC 2040
CCCTCCCCAA GAAGGGAGGG GGCTACTTCA GGCCCTTCTG TGTGTTGCCT GGCAGGATAC 2100
CTTGTC AAC CAGCTACCCA CCTCAACTCC CCTGTAGTTT AGGACACAAA ACAGCTACCA 2160
GCGGTACAGA GCGGTGATCA AAGCCGAGTA CTTACA ACTC TGGTAAGCCT AGCTTCTCCG 2220
CCTCAGCCCT TCTGCTTCTG GAAGGGCTAT CCTGGGGGTG AACTTGAAAC TCTCATCAGG 2280
CTTCTG CAAA AGCTCTTCTT CCTGAAGACA GACCCAGCCT TTGTGCTCTC ACCCTCCACT 2340
CTGGTAAAGC TGCACCTCTG GGGGAATGAG GGGCTGCAGG AATCTCTGGA GAGCCTGGTG 2400
CTTCACGATG CTGCTCTGGT GATTCTTGTA CCTAATCTGG TGTGCTCACC AATGAGTGAA 2460
AGGGATCGTG GGT CAGGGAC ACCGAGAGAG TGAGGTCACT TCCACTTCAA ACCTTCAGTG 2520
AGGGGGTGGG ATGGAGAGAA TGCTGAATCT TTTTTTTGAC GGGATGGGGT TTTTCTCTTT 2580
GTAATTATTT CTTTAGTTTA ATTAACCTTT TGGTTGTTTG TGCAATATTA TATATTTTAA 2640
ATTATAATGC ATCTCCCCAG AGTATTTTGT AGCTGGGAAA AGAAAAAGG AAAAAAGAA 2700
AAAAAGATTC TAACAGCTGT TAGTTTTATA ATTAAAAAAG AAAGAAAAAA GAAC TTTGTC 2760
CTGAACCTTT TACAGACTTG CCGTTAACAG CATTAAAGTG ATTCACCC 2808

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 717 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: ADRETUT06
 (B) CLONE: 2821925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140 :

CATGCGCCGA CCTTCCTCGG CTGGATTTAC ANGTTNNCCC TTAACACCCG GGATTTAAGG 60
GACCCACACT ACCTTCCCGA AGTTGAAGGC AAGCGGTGAT TGTGTGTAGA CGGCGCTTTG 120
TCATGGGACC TGTGCGGTTG GGAATATTGC TTTTCCTTTT TTTGGCCGTG CACGAGGCTT 180
GGGCTGGGAT GTTGAAGGAG GAGGACGATG ACACAGAACG CTTGCCCAGC AAATGCGAAG 240
TGTGTAAGCT GCTGAGCACA GAGCTACAGG CGGAACTGAG TCGCACCGGT CGATCTCGAG 300
AGGTGCTGGA GCTGGGGCAG GTGCTGGATA CAGGCAAGAG GAAGAGACAC GTGCCTTACA 360
GCGTTTCAGA GACAAGGCTG GAAGAGGCCCT TAGAGAATTT ATGTGAGCGG ATCCTGGACT 420
ATAGTGTTCA CGCTGAGCGC AAGGGCTCAC TGAGATATGC CAAGGGTCAG AGTCAGACCA 480
TGGCAACACT GAAAGGCCTA GTGCAGAAGG GGGTGAAGGT GGATCTGGGG ATCCCTCTGG 540
AGCTTTTGGG ATGAGCCCAG CCGTTGAGGT CACATACCTC AAGAAGCAGT GTGAGACCAT 600
GTTNGAGGAG TTTTGAGACA TTGTGGGAGA CTGGTACTTG CACCATCAGG AGCAGCCGCT 660
ACAAGATTTT CTCTGTGAAG GTCATGTGCT GCCAGCTGCT TGAAGTGCAT GTCGGGT 717

(2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2552 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: UTRSTUT05
 (B) CLONE: 2879068

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141 :

GGCAGGGGGC GCGCCGGGCC CAGCGCCACG TCACCGCCCA GCAGCCCTCC CGATTGGCGG 60
GCGGGGCGGC TATAAAGGGA GGGCGCAGGC GGCGCCCGGA TCTCTTCCGC CGCCATTTTA 120

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AATCCAGCTC CATAACAACGC TCCGCCGCCG CTGCTGCCGC GACCCGGACT GCGCGCCAGC 180
ACCCCCCTGC CGACAGCTCC GTCACATATGG AGGATATGAA CGAGTACAGC AATATAGAGG 240
AATTCGCAGA GGGATCCAAG ATCAACGCGA GCAAGAATCA GCAGGATGAC GGTAAAATGT 300
TTATTGGAGG CTTGAGCTGG GATACAAGCA AAAAAGATCT GACAGAGTAC TTGTCTCGAT 360
TTGGGGAAGT TGTAGACTGC ACAATTAAAA CAGATCCAGT CACTGGGAGA TCAAGAGGAT 420
TTGGATTTGT GCTTTTCAAA GATGCTGCTA GTGTTGATAA GGTTTTGGAA CTGAAAGAAC 480
ACAAACTGGA TGGCAAATTG ATAGATCCCA AAAGGGCCAA AGCTTTAAAA GGGAAAGAAC 540
CTCCCAAAAA GGTTTTTGTG GGTGGATTGA GCCCGGATAC TTCTGAAGAA CAAATTAAAG 600
AATATTTTGG AGCCTTTGGA GAGATTGAAA ATATTGAACT TCCCATGGAT AAAAAACAA 660
ATGAAAGAAG AGGATTTTGT TTTATCACAT ATACTGATGA AGAGCCAGTA AAAAAATTGT 720
TAGAAAGCAG ATACCATCAA ATTGGTTCTG GGAAGTGTGA AATCAAAGTT GCACAACCCA 780
AAGAGGTATA TAGGCAGCAA CAGCAACAAC AAAAAGGTGG AAGAGGTGCT GCAGCTGGTG 840
GACGAGGTGG TACGAGGGGT CGTGGCCGAG GTCAGGGCCA AACTGGAAC CAAGGATTTA 900
ATAACTATTA TGATCAAGGA TATGGAAATT ACAATAGTGC CTATGGTGGT GATCAAAACT 960
ATAGTGGCTA TGGCGGATAT GATTATACTG GGTATAACTA TGGGA ACTAT GGATATGGAC 1020
AGGGATATGC AGACTACAGT GGCCAACAGA GCACTTATGG CAAGGCATCT CGAGGGGGTG 1080
GCAATCACCA AAACAATTAC CAGCCATACT AAAGGAGAAC ATTGGAGAAA ACAGGTGTGT 1140
ATAAGAGTAC AGGAAAACAG TAGAAATGTC TAATTTAATT TAAAGATCAA TAGACAAATG 1200
AAACGTAAAA ACAAATACT ATGTAGCCTG TTTTACTAA ATTGTTGATT TTTTAATTGC 1260
TTTATGAGCC TGTTTTGCCT AAAGTGTCTA TAGATCTTTA ACTTTAAAGT CTTATCTCAC 1320
TTTCTTTAGT ATTGCAGAAA AACTTAAGAG TTTTCTGTT TGCTTTTGTG TACCAGGTGG 1380
TCTAGAGGAA TAATTAAACA TTTTAGAACT ATTAACAGGT AAAGTACTGA AATGGGTACA 1440
ACTTAAGGAA AACAAGAATG TTGTCTTCTA ACTCTGACAT TATACCTTGT TTGTACCCGC 1500
CAGCGGGAAC TTCATTGCAG GCCGTGTGTC ACCCTGACCA CGTCTATCTC TGGGGGTCGC 1560
ACGTTGCGGG CAGAGCGCAA GGCATACACC AGAAAACGCT GTCCTGTGGT ATGGTCTCTT 1620
CCAACTTCAT GTACCAGCGT AAAGATTAAA GTGGAAA ACT TCAGACTTTG GCTTCATTTT 1680
TAATCTTTTT GGAGATTAAG TGTCTAACT TAACTTAAAT GGTTTTTTAC AGGAGTTAAA 1740
GTACATAAAT GCCTTTTTTAC AGCTTAATCA TTTTGGTCTT CTGTTTAGTG TTGTATTTCA 1800
ATTGTGGAGC CTCATTTTAA GTGTTCATTC TTTTAAGATT TAATGCTTGC TTTTCTTTT 1860
TATAGCTAAT AGTGAAATCT ACAAACCAA ACAAGA ACTT TTAAATCTGG GATATAAATT 1920
AAAGATCATA TGCACAGATC AATTTATGTT CTTGTAATAA ACTTATTAGA AATTGGTGTT 1980

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TGTGATAGCA TTTTACTTGG GTTACTAGAG ATGCTTCTAG TAGACCTTAA TCTAGCATAG 2040
TTGAACCTCT GAATATGGGA AGGTTGTATT CCCAGATTCT TTCCTGAATA GATTTGAATT 2100
TAATGTCATT TGGGAACTCC AGGGTGAGTT TATTGACTAC CCAAAGTGTG TTTTACCAAT 2160
AAATATGCAT ATGATCTTTA ATTATTGAAG AAAATAAAGT GAGGACTTAA AACAATTCAT 2220
GAAAGTGGAC CTTTAAAAGC TTGTCAGAGT TGCACAAATC TAACTGGTAT TTTGTTTTTG 2280
TTTTTAGGAG GAGATGTTAA AGTAACCCAT CTTGCAGGAC GACATTGAAG ATTGGTCTTC 2340
TGTTGATCTA AGATGATTAT TTTGTAAAAG ACTTTCTAGT GTACAAGACA CCATTGTGTC 2400
CAACTGTATA TAGCTGCCAA TTAGTTTTCT TTGTTTTTAC TTTGTCCTTT GCTATCTGTG 2460
TTATGACTCA ATGTGGATTT GTTTATACAC ATTTTATTG TATCATTTCA TGTTAAACCT 2520
CAAATAAATG CTTCTTATG TGAAAAAAAA AA 2552

(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1046 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SINJNOT02
- (B) CLONE: 2886757

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142 :

TACCAGTGTA AAGCCAGAGC TGAGGTTCTT GATAGTCCAC AATGGGTGAA CCACAGCAAG 60
TGAGTGCACCT TCCACCACCT CCAATGCAAT ATATCAAGGA ATATACGGAT GAAAATATTC 120
AAGAAGGCTT AGCTCCCAAG CCTCCCCCTC CAATAAAAGA CAGTTACATG ATGTTTGGCA 180
ATCAGTTCCA ATGTGATGAT CTTATCATCC GCCCTTTGGA AAGTCAGGGC ATCGAACGGC 240
TTCATCCTAT GCAGTTTGAT CACAAGAAAG AACTGAGAAA ACTTAATATG TCTATCCTTA 300
TTAATTTCTT GGACCTTTTA GATATTTTAA TAAGGAGCCC TGGGAGTATA AAACGAGAAG 360
AGAAACTAGA AGATCTTAAG CTGCTTTTTG TACACGTGCA TCATCTTATA AATGAATACC 420
GACCCACCA AGCAAGAGAG ACCTTGAGAG TCATGATGGA GGTCCAGAAA CGTCAACGGC 480
TTGAAACAGC TGAGAGATTT CAAAAGCACC TGAACGAGT AATTGAAATG ATTCAGAATT 540
GCTTGGCTTC TTTGCCTGAT GATTTGCCTC ATTCAGAAGC AGGAATGAGA GTAAAACTG 600
AACCAATGGA TGCTGATGAT AGCAACAATT GTACTGGACA GAATGAACAT CAAAGAGAAA 660
ATTCAGGTCA TAGGAGAGAT CAGATTATAG AGAAAGATGC TGCCTTGTGT GTCCTAATTG 720

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ATGAGATGAA TGAAAGACCA TGAAAGATGT TTCTTTTTCT TTTTTCCTT TTGATAATAG 780
CATCATATAT TAGTTCATTT TCTTTTGGAC AGTCTTAAGA GAAGTTTCAC TAAAAATGTA 840
AACAGCTTTA ATCTTGACTC CAAATTTTTC AATTATGAGA TGTCATAGGC AGTAATTTTCG 900
CTGTATAACA AGCATAGACA AATGAGTGTC CCTGCACTAA GAAGAATCAC TTTAAAAAGC 960
AAAGTGTTAG CTGCTGTTGT ATGGGACATT CCTATGTTTT AGAGTTGCAG TAAAACTTTG 1020
ATGATAACCT CAAAAAAAAA TAAAAA 1046

(2) INFORMATION FOR SEQ ID NO: 143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1864 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SCORNOT04
- (B) CLONE: 2964329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143 :

GCCCTGGGCT CGCGGCGGTG CCGCGGGGAT GGCGGGAGCC GGAGCTGGAG CCGGAGCTCG 60
CGGCGGAGCG GCGGCGGGGG TCGAGGCTCG AGCTCGCGAT CCACCGCCCG CGCACC GCGC 120
ACATCCTCGC CACCCTCGGC CTGCGGCTCA GCCCTCGGCC CGCAGGATGG ATGGCGGGTC 180
AGGGGGCCTG GGGTCTGGGG ACAACGCCCC GACCACTGAG GCTCTTTTCG TGGCACTGGG 240
CGCGGGCGTG ACGGCGCTCA GCCATCCCCT GCTCTACGTG AAGCTGCTCA TCCAGGTGGG 300
TCATGAGCCG ATGCCCCCA CCCTTGGGAC CAATGTGCTG GGGAGGAAGG TCCTCTATCT 360
GCCGAGCTTC TTCACCTACG CCAAGTACAT CGTGCAAGTG GATGGTAAGA TAGGGCTGTT 420
CCGAGGCCTG AGTCCCCGGC TGATGTCCAA CGCCCTCTCT ACTGTGACTC GGGGTAGCAT 480
GAAGAAGGTT TTCCCTCCAG ATGAGATTGA GCAGTTTCC AACAAGGATG ATATGAAGAC 540
TTCCCTGAAG AAAGTTGTGA AGGAGACCTC CTACGAGATG ATGATGCAGT GTGTGTCCCG 600
CATGTTGGCC CACCCCCTGC ATGTCATCTC AATGCGCTGC ATGGTCCAGT TTGTGGGACG 660
GGAGGCCAAG TACAGTGGTG TGCTGAGCTC CATTGGGAAG ATTTTCAAAG AGGAAGGGCT 720
GCTGGGATTC TTCGTTGGAT TAATCCCTCA CCTCCTGGGC GATGTGGTTT TCTTGTGGGG 780
CTGTAACCTG CTGGCCCACT TCATCAATGC CTACCTGGTG GATGACAGCT TCAGCCAGGC 840
CCTGGCCATC CGGAGCTATA CCAAGTTCGT GATGGGGATT GCAGTGAGCA TGCTGACCTA 900
CCCCCTCCTG CTAGTTGGCG ACCTCATGGC TGTGAACAAC TCGGGGCTGC AAGCTGGGCT 960

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CCCCCCTTAC TCCCCAGTGT TCAAATCCTG GATTCACTGC TGGAAGTACC TGAGTGTGCA 1020
GGGCCAGCTC TTCCGAGGCT CCAGCCTGCT TTTCCGCCGG GTGTCATCAG GATCGTGCTT 1080
TGCCCTGGAG TAACCTGAAT CATCTAAAAA ACACGGTCTC AACCTGGCCA CCGTGGGTGA 1140
GGCCTGACCA CCTTGGGACA CCTGCGAGAC GACTCCAACC CAACAACAAC CAGATGTGCT 1200
CCAGCCCAGC CGGGCTTCAG TTCCATATTT GCCATGTGTC TGTCCAGATG TGGGGTTGAG 1260
CGGGGGTGGG GCTGCACCCA GTGGATTGGG TCACCCGGCA GACCTAGGGA AGGTGAGGCG 1320
AGGTGGGGAG TTGGCAGAAT CCCCATACCT CGCAGATTG CTGAGTCTGT CTTGTGCAGA 1380
GGGCCAGAGA ATGGCTTATG GGGGCCCAGG TTGGATGGGG AAAGGCTAAT GGGGTCAGAC 1440
CCCACCCCGT CTACCCCTCC AGTCAGCCCA GCGCCCATCC TGCAGCTCAG CTGGGAGCAT 1500
CATTCTCCTG CTTTGTACAT AGGGTGTGGT CCCCTGGCAC GTGGCCACCA TCATGTCTAG 1560
GCCTATGCTA GGAGGCAAAT GGCCAGGCTC TGCCTGTGTT TTTCTCAACA CTACTTTTCT 1620
GATATGAGGG CAGCACCTGC CTCTGAATGG GAAATCATGC AACTACTCAG AATGTGTCTT 1680
CCTCATCTAA TGCTCATCTG TTTAATGGTG ATGCCTCGCG TACAGGATCT GGTTACCTGT 1740
GCAGTTGTGA ATACCAGAG GTTGGGCAGA TCAGTGTCTC TAGTCCTACC CAGTTTTTAA 1800
GTTTCATGGTA AGATTGACC TCATCTCCCG CAAATAAATG TATTGGTGAT TTGGAAAAAA 1860
AAAA 1864

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SCORNOT04
- (B) CLONE: 2965248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144 :

GTCTGCAGCT CCGGCCGCCA CTTGCGCCTC TCCAGCCTCC GCAGGCCCAA CCGCCGCCAG 60
CACCATGGCC AGCACCATTT CCGCCTACAA GGAGAAGATG AAGGAGCTGT CCGTGCTGTC 120
GCTCATCTGC TCCTGCTTCT ACACACAGCC GCACCCCAAT ACCGTCTACC AGTACGGGGA 180
CATGGAGGTG AAGCAGCTGG ACAAGCGGGC CTCAGGCCAG AGCTTCGAGG TCATCCTCAA 240
GTCCCCTTCT GACCTGTCCC CAGAGAGCCC TATGCTCTCC TCCCCACCA AGAAGAAGGA 300
CACCTCCCTG GAGGAGCTGC AAAAGCGGCT GGAGGCAGCC GAGGAGCGGA GGAAGACGCA 360

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GGAGGCGCAG GTGCTGAAGC AGCTGGCGGA CGGCGCGAGC ACGAGCGCGA GGTGCTGCAC 420
AAGGCGCTGG AGGAGAATAA CAACTTCAGC CGCCAGGCGG AGGAGAAGCT CAACTACAAG 480
ATGGAGCTCA GCAAGGAGAT CCGCGAGGCA CACCTGGCCG CACTGCGCGA GCGGCTGCGC 540
GAGAAGGAGC TGCACGCGGC CGAGGTGCGC AGGAACAAGG AGCAGCGAGA AGAGATGTCTG 600
GGCTAAGGGC CCGGGACGGG CGGCGCCCAT CCTGCGACGG AACACGTTCG GGTTTTGGTT 660
TTGTTTCGTT CACCTCTGTC TAGATGCAAC TTTTGTTCCT CCTCCCCAC CCCAGCCCCC 720
AGCTTCATGC TTCTCTTCCG CACTCAGCCG CCCTGCCCTG TCCTCGTGGT GAGTCGCTGA 780
CCACGGCTTC CCCTGCAGGA GCCGCCGGGC GTGAGACGCG GTCCCTCGGT GCAGACACCA 840
GGCCGGGCGC GGCTGGGTCC CCCGGGGGCC CTGTGAGAGA GGTGGTGGTG ACCGTGGTAA 900
ACCCAGGGCG GTGGCGTGGG ATCGCGGGTC CTTACGCTGG GCTGTCTGGT CAGCACGTGC 960
AGGTCAGGGC AGGTCTCTG AGCCGGCGCC CCTGGCCAGC AGGCGAGGCT ACAGTACCTG 1020
CTGTCTTTCC AGGGGAAGG GGCTCCCCAT GAGGGAGGGG CGACGGGGGA GGGGGGTGAT 1080
GGTGCTGGG AGCCTGCGTG TGCAGCCGGT GCTTGTGAA CTGGCAGGCG GGTGGGTGGG 1140
GGCTGCAGCT TTCCTTAATG TGGTTGCACA GGGTCTCTT GAGACCACCT GGCGTGAGGT 1200
GGACACCCTG GGCCTTCCTG GAAGCCTGCA GTTGGGGGCC TGCCCTGAGT CTGCTGGGGA 1260
GTGGGCATTC TCTGCCAGGG ACCCATGAGC AGGCTGCATG GTCTAGAGGT TGTGGGCAGC 1320
ATGGACAGTC CCCCACTCAG AAGTGCAAGA GTTCCAAAGA GCCTCTGGCC CAGGCCCCCTC 1380
CGTGGGACAG CCCCGCCGCC CCTCCCCACC AGGGCTTTGC AGATGTCCTT GAAAGACCCA 1440
CCCTAGAGCC CTTTGAGTG CTGGCCCCCTC CTGTGCCCTC TGCCCTGGTG GAAGCGGCAG 1500
CCACAAGTCC TCCTCAGGGA GCCCCAAGGG GGATTTTGTG GGACCGCTGC CCACAGATCC 1560
AGGTGTTGGA AGGGCAGCGG GTAAGGTTCC CAAGCCAGCC CCAACACCCT TCCCACTTGG 1620
CACCCAGAGG GGGCTGTGGG TGGAGGCCTG ACTCCAGGCC TCTCCTGCCC ACACCCTCTG 1680
GGCTGAGTTC CTTCTTTCCC TTGGACGCC AGTGCTGGCC TTGGAGGACG GTCAGCTGGA 1740
GGATGGCGGT GGGGGAGGCT GTCTTTGTAC CACTGCAGCA TCCCCACTT CTCCACGGAA 1800
GCCCCATCCC AAAGCTGCTG CCTGGCCCCCT TGCTGTAAAG TGTGAAGGGG GCGGCTGAGT 1860
TCTCTTAGGA CCCAGAGCCA GGGCCCTCAA CTTCCATCCT GCGGGAGGCC TTGGCCGGGC 1920
ACTGCCAGTG TCTTCCAGAG CCACACCCAG GGACCACGGG AGGATCCTGA CCCCTGCAGG 1980
GCTCAGGGGT CAGCAGGGAC CCACTGCCCC ATCTCCCTCT CCCACCAAG ACAGCCCCAG 2040
AAGGAGCAGC CAGCTGGGAT GGGAAACCAA GGCTGTCCAC ATCTGGCTTT TGTGGGACTC 2100
AGAAAGGGAA GCAGAACTGA GGGCTGGGAT ATCCTCATG GTGGCAGCGC TCATAGCGAA 2160
AGCCTACTGT AATATGCACC CATCTCATCC ACGTAGTAAA GTGAACTTAA AAATTCAATC 2220

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AAATGAACAA TTAAATAAAC ACCTGTGTGT TTAAGACAAA ATAAAAATGG AGGAGAACAA 2280
AAAAAAAGGG GCGGT 2295

(2) INFORMATION FOR SEQ ID NO: 145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 842 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: TLYMNOT06
- (B) CLONE: 3000534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145 :

CGGGGACGGA AGCAGCCCCT GGGCCCGAGG GGCTCGAGGC CGGGCCGGGG CGATGTGGAG 60
CGCGGGCCGC GCGGGGGCTG CCTGGCCGGT GCTGTTGGGG CTGCTGCTGG CGCTGTTAGT 120
GCCGGGCGGT GGTGCCGCCA AGACCGGTGC GGAGCTCGTG ACCTGCGGGT CGGTGCTGAA 180
GCTGCTCAAT ACGCACCACC GCGTGC GGCT GCACTCGCAC GACATCAAAT ACGGATCCGG 240
CAGCGGCCAG CAATCGGTGA CCGGCGTAGA GGCGTCGGAC GACGCCAATA GCTACTGGCG 300
GATCCGCGGC GGCTCGGAGG GCGGGTGCCC GCGCGGGTCC CCGGTGCGCT GCGGGCAGGC 360
GGTGAGGCTC ACGCATGTGC TTACGGGCAA GAACCTGCAC ACGCACC ACT TCCCGTCGCC 420
GCTGTCCAAC AACCAGGAGG TGAGTGCCTT TGGGGAAGAC GGCGAGGGCG ACGACCTGGA 480
CCTATGGACA GTGCGCTGCT CTGGACAGCA CTGGGAGCGT GAGGCTGCTG TGCGCTTCCA 540
GCATGTGGGC ACCTCTGTGT TCCTGT CAGT CACGGGTGAG CAGTATGGAA GCCCCATCCG 600
TGGGCAGCAT GAGGTCCACG GCATGCCCAG TGCCAACACG CACAATACGT GGAAGGCCAT 660
GGAAGGCATC TTCATCAAGC CTAGTGTGGA GCCCTCTGCA GGTCACGATG AACTCTGAGT 720
GTGTGGATGG ATGGGTGGAT GGAGGGTGGC AGGTGGGGCG TCTGCAGGGC CACTCTTGGC 780
AGAGACTTTG GGT TTGTAGG GGTCCTCAAG TGCCTTTGTG ATTAAAGAAT GTTGGTCTAA 840
AA 842

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2345 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: HEAANOT01
(B) CLONE: 3046870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146 :

GTCCCGCCCC GCAGCTGCGC GCAGGCGCTC GACGAGCCGC TCGCATTCTA CGTAACGGAC 60
GGCGGAGGCT ACGTGAAGAG AGGCGCGGCG TGA CTGAGCT ACGGTTCTGG CTGCGTCCTA 120
GAGGCATCCG GGGCAGTAAA ACCGCTGCGA TCGCGGAGGC GGCGGCCAGG CCGAGAGGCA 180
GGCCGGGCGAG GGGTGTCTGA CGCAGGGCGC TGGGCGGGGT TTCGGCTTCG GCCACAGCTT 240
TTTTTCTCAA GGTGCAATGA AAGCCTTCCA CACTTTCTGT GTTGTCTTC TGGTGTCTTG 300
GAGTGTCTCT GAAGCCAAGT TTGATGATTT TGAGGATGAG GAGGACATAG TAGAGTATGA 360
TGATAATGAC TTCGCTGAAT TTGAGGATGT CATGGAAGAC TCTGTTACTG AATCTCCTCA 420
ACGGGTCATA ATCACTGAAG ATGATGAAGA TGAGACCACT GTGGAGTTGG AAGGGCAGGA 480
TGAAAACCAA GAAGGAGATT TTGAAGATGC AGATACCCAG GAGGGAGATA CTGAGAGTGA 540
ACCATATGAT GATGAAGAAT TTGAAGGTTA TGAAGACAAA CCAGATACTT CTTCTAGCAA 600
AAATAAAGAC CCAATAACGA TTGTTGATGT TCCTGCACAC CTCCAGAACA GCTGGGAGAG 660
TTATTATCTA GAAATTTTGA TGGTGA CTGCTGCT TATATCATGA ATTACATCAT 720
TGGGAAGAAT AAAAACAGTC GCCTTGACAC GGCCTGGTTT AACACTCATA GGGAGCTTTT 780
GGAGAGCAAC TTTACTTTAG TGGGGGATGA TGGA ACTAAC AAAGAAGCCA CAAGCACAGG 840
AAAGTTGAAC CAGGAGAATG AGCACATCTA TAACCTGTGG TGTCTGGTC GAGTGTGCTG 900
TGAGGGCATG CTTATCCAGC TGAGGTTCTT CAAGAGACAA GACTTACTGA ATGTCCTGGC 960
CCGGATGATG AGGCCAGTGA GTGATCAAGT GCAAATAAAA GTAACCATGA ATGATGAAGA 1020
CATGGATACC TACGTATTTG CTGTTGGCAC ACGGAAAGCC TTGGTGGCAG TACAGAAAGA 1080
GATGCAGGAT TTGAGTGAGT TTTGTAGTGA TAAACCTAAG TCTGGAGCAA AGTATGGACT 1140
GCCGGACTCT TTGGCCATCC TGTCAGAGAT GGGAGAAGTC ACAGACGGAA TGATGGATAC 1200
AAAGATGGTT CACTTTCTTA CACACTATGC TGACAAGATT GAATCTGTTC ATTTTTCAGA 1260
CCAGTTCTCT GGTCCAAAAA TTATGCAAGA GGAAGGTCAG CCTTTAAAGC TACCTGACAC 1320
TAAGAGGACA CTGTTGTTTA CATTAAATGT GCCTGGCTCA GGTAACACTT ACCCAAAGGA 1380
TATGGAGGCA CTGCTACCCC TGATGAACAT GGTGATTTAT TCTATTGATA AAGCCAAAAA 1440
GTTCCGACTC AACAGAGAAG GCAAACAAAA AGCAGATAAG AACC GTGCCC GAGTAGAAGA 1500
GAACTTCTTG AAAGTGACAC ATGTGCAAAG ACAGGAAGCA GCACAGTCTC GGCGGGAGGA 1560

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GAAGAAAAAGA GCAGAGAAGG AGCGAATCAT GAATGAGGAA GATCCTGAGA AACAGCGCAG 1620
GCTGGAGGAG GCTGCATTGA GGCCTGAGCA AAAGAAGTTG GAAAAGAAGC AAATGAAAAT 1680
GAAACAAATC AAAGTGAAAG CCATGTAAAG CCATCCCAGA GATTTGAGTT CTGATGCCAC 1740
CTGTAAGCTC TGAATTCACA GGAAACATGA AAAACGCCAG TCCATTTCTC AACCTTAAAT 1800
TTCAGACAGT CTTGGGCAAC TGAGAAATCC TTATTTTCATC ATCTACTCTG TTTGGGGTTT 1860
GGGGTTTTAC AGAGATTGAA GATACCTGGA AAGGGCTCTG TTTCAAGAAT TTTTTTTTCC 1920
AGATAATCAA ATTATTTTGA TTATTTTATA AAAGGAATGA TCTATGAAAT CTGTGTAGGT 1980
TTTAAATATT TTAATAATTA TAATACAAAT CATCAGTGCT TTTAGTACTT CAGTGTTTAA 2040
AGAAATACCA TGAAATTTAT AGGTAGATAA CCAGATTGTT GCTTTTTTGTT TAAACCAAGC 2100
AGTTGAAATG GCTATAAAGA CTGACTCTAA ACCAAGATTC TGCAAATAAT GATTGGAATT 2160
GCACAATAAA CATTGCTTGA TGTTTTCTTG TATGTCTACA TTAAACTTGA GAAAAAGTAA 2220
AAATTAGAAC ACTGTATGTA GTAATGAAAT TTCAGGGACC CAGAACATAA TGTAGTATAT 2280
GTTTTTAGGT GGGAGATGCT GATAACAAAA TTAATAGGAA GTCTGTAGGC ATTAGGATAC 2340
TGACA 2345

(2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PONSATZ01
- (B) CLONE: 3057669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147 :

CCCACGCGTC CGCCACGCG TCCGTTTTCA GTAGGGATTT CCTGTGACCA GACAAGTTCA 60
TCTGAGAGCC AGTTCTCACC ACTGGAATTC TCAGGAATGG ACCATGAGGA CATCAGTGAG 120
TCAGTGGATG CAGCATACAA CCTCCAGGAC AGTTGCCTTA CAGACTGTGA TGTGGAAGAT 180
GGGACTATGG ATGGCAATGA TGAGGGGCAC TCCTTTGAAC TTTGTCCTTC TGAAGCTTCT 240
CCTTATGTAA GGTCAAGGGA GAGAACCTCC TCTTCAATAG TATTTGAAGA TTCTGGCTGT 300
GATAATGCTT CCAGTAAAGA AGAGCCGAAA ACTAATCGAT TGCATATTGG CAACCATTGT 360
GCTAATAAAC TAACTGCTTT CAAGCCCACC AGTAGCAAAT CTTCTTCTGA AGCTACATTG 420
TCTATTTCTC CTCCAAGACC AACCACCTTA AGTTTAGATC TCACTAAAAA CACCACAGAA 480

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AAACTCCAGC CCAGTTCACC AAAGGTGTAT CTTTACATTC AAATGCAGCT GTGCAGAAAA 540
GAAAACCTCA AAGACTGGAT GAATGGACGA TGTACCATAG AGGAGAGAGA GAGGAGCGTG 600
TGTCTGCACA TCTTCCTGCA GATCGCAGAG GCAGTGGAGT TTCTTCACAG TAAAGGACTG 660
ATGCACAGGG ACCTCAAGCC ATCCAACATA TTCTTTACAA TGGATGATGT GGTCAAGGTT 720
GGAGACTTTG GGTTAGTGAC TGCAATGGAC CAGGATGAGG AAGAGCAGAC GGTTCGACC 780
CCAATGCCAG CTTATGCCAG ACACACAGGA CAAGTAGGGA CCAAAGTGT TATGAGCCCA 840
GAGCAGATTC ATGGAAACAG CTATTCTCAT AAAGTGGACA TCTTTTCTTT AGGCCTGATT 900
CTATTTGAAT TGCTGTATCC ATTCAGCACT CAGATGGAGA GAGTCAGGAC CTTAACTGAT 960
GTAAGAAATC TCAAATTTCC ACCATTATTT ACTCAGAAAT ATCCTTGTGA GTACGTGATG 1020
GTTCAAGACA TGCTCTCTCC ATCCCCCATG GAACGACCTG AAGCTATAAA CATCATTGAA 1080
AATGCTGTAT TTGAGGACTT GGACTTTCCA GGAAAAACAG TGCTCAGACA GAGGTCTCGC 1140
TCCTTGAGTT CATCGGGAAC AAAACATTCA AGACAGTCCA ACAACTCCCA TAGCCCTTTG 1200
CCAAGCAATT AGCCTTAAGT TGTGCTAGCA ACCCTAATAG GTGATGCAGA TAATAGCCTA 1260
CTTCTTAGAA TATGCCTGTC CAAAATTGCA GACTTGAAAA GTTTGTTCTT CGCTCAATTT 1320
TTTTGTGGAC TACTTTTTTT ATATCAAATT TAAGCTGGAT TTGGGGGCAT AACCTAATTT 1380
GAGCCAACTC CTGAGTTTTG CTATACTTAA GGAAAGGGCT ATCTTTGTTC TTTGTTAGTC 1440
TCTTGAAACT GGCTGCTGGC CAAGCTTTAT AGCCCTCACC ATTTGCCTAA GGAGGTAGCA 1500
GCAATCCCTA ATATATATAT ATAGTGAGAA CTAAAATGGA TATATTTTTA TAATGCAGAA 1560
GAAGGAAAGT CCCCCTGTGT GGTAAGTGT TGTCTCTAGA AATATGCTTT CTAGAGATAT 1620
GATGATTTTG AACTGATTT CTAGAAAAAG CTGACTCCAT TTTTGTCCCT GGCGGGTAAA 1680
TTAGGAATCT GCACTATTTT GGAGGACAAG TAGCACAAAC TGTATAACGG TTTATGTCCG 1740
TAGTTTTATA GTCCTATTTG TAGCATTCAA TAGCTTTATT CCTTAGATGG TTCTAGGGTG 1800
GGTTTACAGC TTTTGTACT TTTACCTCCA ATAAAGGGAA AATGAAGCTT TTTATGTAAA 1860
TTGGTTGAAA GGTCTAGTTT TGGGAGGAAA AAAGCCGTAG TAAGAAATGG ATCATATATA 1920
TTACAACATA CTTCTTCAAC TATGGACTTT TTAAGCCTAA TGAAATCTTA AGTGTCTTAT 1980
ATGTAATCCT GTAGGTTGGT ACTTCCCCCA AACTGATTAT AGGTAACAGT TTAATCATCT 2040
CACTTGCTAA CATGTTTTTA TTTTTCCTG TAAATATGTT TATGTTTTAT TTATAAAAAT 2100
TCTGAAATCA ATCCATTTGG GTTGGTGGTG TACAGAACAC ACTTAAGTGT GTTAACTTGT 2160
GACTTCTTTC AAGTCTAAAT GATTTAATAA AACTTTTTTT AAATTAAAAA AAAAA 2215

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(2) INFORMATION FOR SEQ ID NO: 148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: HEAONOT03
- (B) CLONE: 3088178

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148 :

GGTTGACATG ATGAACAATC GGTTTCGGAA GGATATGATG AAAAATGCTA GTGAAAGTAA 60
ACTTTCGAAA GACAACCTTA AAAAGAGACT TAAAGAAGAA TTCCAACATG CCATGGGAGG 120
AGTACCTGCC TGGGCAGAGA CTAATAAGCG GAAAACATCT TCAGATGATG AAAGTGAAGA 180
GGATGAAGAT GATTTGTTGC AAAGGACTGG GAATTCATA TCCACATCAA CTTCTCTTCC 240
AAGAGGCATC TTGAAGATGA AGAACTGCCA GCATGCGAAT GCTGAACGTC CTACTGTTGC 300
TCGGATCTCA TCTGTGCAGT TCCATCCCGG TGCACAGATT GTGATGGTTG CTGGATTAGA 360
TAATGCTGTA TCACTATTTT AGGTTGATGG GAAAACAAAT CCTAAAATTC AGAGCATCTA 420
TTTGAAAAGG TTTCCAATCT TTAAGGCTTG TTTTAGTGCT AATGGGGAAG AAGTTTTAGC 480
CACGAGTACC CACAGCAAGG TTCTTTATGT CTATGACATG CTGGCTGGAA AGTTAATTCC 540
TGTGCATCAA GTGAGAGGTT TGAAAGAGAA GATAGTGAGG AGCTTTGAAG TCTCCCCAGA 600
TGGGTCCTTC TTGCTCATAA ATGGCATTGC TGGATATTTG CATTTGCTAG CAATGAAGAC 660
CAAAGAACTG ATTGGAAGCA TGAAAATTAA TGGAAGGGTT GCAGCATCCA CATTCTCTTC 720
AGATAGTAAG AAAGTATACG CCTCTTCGGG GGATGGAGAA GTTTATGTTT GGGATGTGAA 780
CTCAAGGAAG TGCCTTAACA GATTTGTTGA TGAAGGCAGT TTATATGGAT TAAGCATTGC 840
CACATCTAGG AATGGACAGT ATGTTGCTTG TGGTTCTAAT TGTGGAGTGG TAAATATATA 900
CAATCAAGAT TCTTGTCTCC AAGAAACAAA CCCAAAGCCA ATAAAAGCTA TAATGAACCT 960
GGTTACAGGT GTTACTTCTC TGACCTTCAA TCCTACTACA GAAATCTTGG CAATTGCTTC 1020
AGAAAAAATG AAAGAAGCAG TCAGATTGGT TCATCTTCCT TCCTGTACAG TATTTTCAAA 1080
CTTCCCAGTC ATTAAAAATA AGAATATTTT TCATGTTTAT ACCATGGATT TTTCTCCGAG 1140
AAGTGGATAC TTTGCCTTGG GGAATGAAAA GGGCAAGGCC CTGATGTATA GGTTGCACCA 1200
TACTCAGAC TTCTAAAGAG ACTATTTGAA GTCCAGTTGA GTCACAAGAG AAGCCTGTCT 1260
TGATATATCA TCTCAGAAAC TTTCTGAAT ATGTGATAAT ATATGAAAAA TGATTTATAG 1320
ATCCAGCTGT GCTTAAGAGC CAGTAATGTC TTAATAAACA TGTGGCAGCT TTTGTTTGAA 1380
AAAAAAAAAA AAAGG 1395

(2) INFORMATION FOR SEQ ID NO: 149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2609 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTNOT19
- (B) CLONE: 3094321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149 :

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CCCCCCATGG CACTGTCGCG GGGGCTGCCC CGGGAGCTGG CTGAGGCGGT GGCCGGGGGC 60
CGGGTGCTGG TGGTGGGGGC GGGCGGCATC GGCTGCGAGC TCCTCAAGAA TCTCGTGCTC 120
ACCGGTTTCT CCCACATCGA CCTGATTGAT CTGGATACTA TTGATGTAAG CAACCTCAAC 180
AGACAGTTTT TGTTCAAAA GAAACATGTT GGAAGATCAA AGGCACAGGT TGCCAAGGAA 240
AGTGTAAGTC AGTTTTACCC GAAAGCTAAT ATCGTTGCCT ACCATGACAG CATCATGAAC 300
CCTGACTATA ATGTGGAATT TTTCCGACAG TTTATACTGG TTATGAATGC TTTAGATAAC 360
AGAGCTGCCC GAAACCATGT TAATAGAATG TGCCTGGCAG CTGATGTTCC TCTTATTGAA 420
AGTGGAACAG CTGGGTATCT TGGACAAGTA ACTACTATCA AAAAGGGTGT GACCGAGTGT 480
TATGAGTGTC ATCCTAAGCC GACCCAGAGA ACCTTTCCTG GCTGTACAAT TCGTAACACA 540
CCTTCAGAAC CTATACATTG CATCGTTTGG GCAAAGTACT TGTTCACCA GTTGTTTGGG 600
GAAGAAGATG CTGATCAAGA AGTATCTCCT GACAGAGCTG ACCCTGAAGC TGCCTGGGAA 660
CCAACGGAAG CCGAAGCCAG AGCTAGAGCA TCTAATGAAG ATGGTGACAT TAAACGTATT 720
TCTACTAAGG AATGGGCTAA ATCAACTGGA TATGATCCAG TTAAACTTTT TACCAAGCTT 780
TTTAAAGATG ACATCAGGTA TCTGTTGACA ATGGACAAAC TATGGCGGAA AAGGAAACCT 840
CCAGTTCCGT TGGACTGGGC TGAAGTACAA AGTCAAGGAG AAGAAACGAA TGCATCAGAT 900
CAACAGAATG AACCCAGTT AGGCCTGAAA GACCAGCAGG TTCTAGATGT AAAGAGCTAT 960
GCACGTCTTT TTTCAAAGAG CATCGAGACT TTGAGAGTTC ATTTAGCAGA AAAGGGGGAT 1020
GGAGCTGAGC TCATATGGGA TAAGGATGAC CCATCTGCAA TGGATTTTGT CACCTCTGCT 1080
GCAAACCTCA GGATGCATAT TTTAGTATG AATATGAAGA GTAGATTGTA TATCAAATCA 1140
ATGGCAGGGA ACATTATTCC TGCTATTGCT ACTACTAATG CAGTAATTGC TGGGTTGATA 1200
GTATTGGAAG GATTGAAGAT TTTATCAGGA AAAATAGACC AGTGCAGAAC AATTTTTTTG 1260
AATAACAAC CAAACCAAG AAAGAAGCTT CTTGTGCCTT GTGCACTGGA TCCTCCCAAC 1320

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CCCAATTGTT ATGTATGTGC CAGCAAGCCA GAGGTGACTG TCGGCTGAA TGTCCATAAA 1380
GTGACTGTTC TCACCTTACA AGACAAGATA GTGAAAGAAA AATTTGCTAT GGTAGCACCA 1440
GATGTCCAAA TTGAAGATGG GAAAGGAACA ATCCTAATAT CTTCCGAAGA GGGAGAGACG 1500
GAAGCTAATA ATCACAAGAA GTTGTGAGAA TTTGGAATTA GAAATGGCAG CCGGCTTCAA 1560
GCAGATGACT TCCTCCAGGA CTATACTTTA TTGATCAACA TCCTTCATAG TGAAGACCTA 1620
GGAAAGGACG TTGAATTTGA AGTTGTTGGT GATGCCCCGG AAAAAGTGGG GCCCAAACAA 1680
GCTGAAGATG CTGCCAAAAG CATAACCAAT GGCAGTGATG ATGGAGCTCA GCCCTCCACC 1740
TCCACAGCTC AAGAGCAAGA TGACGTTCTC ATAGTTGATT CGGATGAAGA AGATTCTTCA 1800
AATAATGCCG ACGTCAGTGA AGAAGAGAGA AGCCGCAAGA GGAAATTAGA TGAGAAAGAG 1860
AATCTCAGTG CAAAGAGGTC ACGTATAGAA CAGAAGGAAG AGCTTGATGA TGTCATAGCA 1920
TTAGATTGAA CAGAAATGCC TCTAAACAGA ACCCTCTTAC TATTTAGTTT ATCTGGGCAG 1980
AACCAGATTG TTATGTCCTT TGTTCCAAAG GGAAAAAATT GACAGCAGTG ACTTGAAAAT 2040
GATTCTGCTC CCTTTGAAAG CATTCAATTTT GCTAGAAGTG TTAGACACAT TGCAGTATGC 2100
TGTATTGAAA GTAGGAATAT AGTTTTAAAA ACCCTTTGAA CAAAGTGTGT GCATAACCAG 2160
TCATGAGATA AAACAACACA ATGCATGTTG CCTTTTTAAT GTAAATACCC TTAGGTATCA 2220
TTAATAGTTT CAAAATATTG TGGTTTAGTA AAGTTGATAC CTGGTTATAA ATATTATGCC 2280
TTTATTTTTG GCTAGAAGAA GAATTATTTT TAGCCTAGAT CTAACCATTT TCATACTCTT 2340
AACTGATTGA AACAGATTCA AAGAAGTATC GAGTGCTATG CATTGAAACT TGTTTTTAAA 2400
TGTTAGATGG CACTATGTAT ATTAATGTAA AACAATGTTA ATTTACTCAA GTTTTCAGTT 2460
TGTACCGCCT GGTATGTCTG TGTAAGAAGC CAATTTTTGT GTATTGTTAC AGTTTCAGGT 2520
TATTTATATT CGATGTTTTG TAAACTCAA ATAACGACTA TACTTATGGA CCAAATAAAT 2580
GGCATCTGCA TTCTTGTTAA AAAAAAAAAA 2609

(2) INFORMATION FOR SEQ ID NO: 150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGTUT13
- (B) CLONE: 3115936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150 :

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CCTGAGGGAT CCACAGAGGG TGCGGTCCTT GGAGGGAGGA CATGCAGTGC CACGTGCCAT 60
GGACCAGCCA GTGGACCCCA TGGCCAGCAA GGCTGCTCCT GGGGCCAGTG GGGTGGACAG 120
TCCCGCCAC GCAGGTGACT GAGGTGCCAG TGTGGGAATG AAAATGCGGC CTGTGCTCCT 180
GGGCCCATGC GTCTCACGCT GCCCTTCCTC TCCAGGGAAG CCTGTGTACC TGCTACTTTT 240
TCCCGAACAA TTCATGGTAA AAACACAAAT GGTATATGGA CAAGATACTG AATGTGGAAG 300
AAACCTACTT GACAGTGTTG GTGAAAATAG GGCCAGGATT TCACACCCGT GAATGCTTTT 360
TACTGAAAAG TATTTTGTGT TTTTCTCCCA GTTACAGAAT GTCTGAAGGG GACAGTGTGG 420
GAGAATCCGT CCATGGGAAA CCTTCGGTGG TGTACAGATT TTTCACAAGA CTTGGACAGA 480
TTTATCAGTC CTGGCTAGAC AAGTCCACAC CCTACACGGC TGTGCGATGG GTCGTGACAC 540
TGGGCCTGAG CTTTGTCTAC ATGATTTCGAG TTTACCTGCT GCAGGGTTGG TACATTGTGA 600
CCTATGCCTT GGGGATCTAC CATCTAAATC TTTTCATAGC TTTTCTTTCT CCCAAAGTGG 660
ATCCTTCCTT AATGGAAGAC TCAGATGACG GTCCTTCGCT ACCCACCAA CAGAACGAGG 720
AATTCCGCCC CTTCAATCGA AGGCTCCCAG AGTTTAAATT TTGGCATGCG GCTACCAAGG 780
GCATCCTTGT GGCTATGGTC TGTACTTTCT TCGACGCTTT CAACGTCCCG GTGTTCTGGC 840
CGATTCTGGT GATGTACTTC ATCATGCTCT TCTGTATCAC GATGAAGAGG CAAATCAAGC 900
ACATGATTAA GTACCGGTAC ATCCCGTTCA CACATGGGAA GAGAAGGTAC AGAGGCAAGG 960
AGGATGCCGG CAAGGCCTTC GCCAGCTAGA AGCGGGACTG AGGCTGCCTC ACGTGTTGCA 1020
AGAACAGTTT TGAGCCATTG TTAACAATGC CTTTTTTCTT CACATAAAGT AGTTGATTAC 1080
GAGGGAGTCA AATTTTCTTT TTA AAAAGGA GCTTCAATGA TTTGTAAGT AAATATCAGG 1140
TTCTAGAAGA AACTGGCGCT TAAACCAAAT CGCATGGATT TCTTTTTCAG TGACGTTCAA 1200
GTGTTTCTCA CGGATGGAAT TCTAGTCAGC TGCAGGCGGG AAGCCAGGCG GGTGGAGCCC 1260
ATGGGAGCAA GGGCGAGTGG CCGGTCCCCG CTGTGCCAGG TGGGCAGGCA GGAGCAAGGC 1320
CTGCGAGGGA GGAACGGGCC GCTCCCCGCC AGCCGCCTTC CCCAGCAGCC GCAGGTGGTG 1380
CCAGCCACTC CACAGAGCCC GAGGGATGAT CTAGCCTGAT TCCTGCGTGT CCGAAAGAAC 1440
TTAACGTTTT AAAGGTGATT GTCAAGTAAC TGTGTGGGGT TCTAATGCCA GTTTCCTAAT 1500
TCCATCTCAC TGGAGATGTT TAAAGTTGGC CTCTATCCTA ATGACTCAA ACTTGTTCT 1560
TAACTACCAT GATTGCTTTT GAGGGCCCGG AATTATAAAT ATATATTATA TTTAATTGT 1620
TTGAGATTAT TTTGACACAT TTCTTTGATA CGTAGAGTGT TTTGTTTTTA ATTTAAATCT 1680
GTCCCTCATG AACCTCCAT GAGGGGCAGC GAAGCTGGCA GGGAGCAGAC TGGCTTTGTA 1740
GGTTCAGCAC TCGGCCCCC ACTGCGGGAG AGGCGGAACC CACTTGCATG TCAGCGTTTT 1800
TGATTGAGA AAAGAAATAC TCTCAACGTT TTACCAAGTG ATTTTACCTC CACCTTTACT 1860

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AAAGTCTTTA CCTAAAACAT GGCAGTCGCT GGACACAGGA AAGCCCACCT TTTGTTTGGC 1920
CTTTTCGAAA GGTGACCCAT ATTGCACAGC AGAACATCAC AGCTGTGGTC CCAGATGAGA 1980
CACTGACATG CGAGTGAAGG CCTCTCCTCC TGGGCCCCGG GCTGCGCAGG CTCCTCACTC 2040
TGGGCGGTGT TTCCTGTCTC AGAATTGACA CGGTGAATGC TTAGTGTCTG GATTTTCTTG 2100
TGCCAGTGTT TACATATCTG ACATCGAGCT CCTCTAAGAG GCCACGTTC AAGCTTGTGTG 2160
TCCCTGACCC AAGATAGCCA GTGCTGCTCC CAGGTGGTAC TTCTGGTACC GTGTTGAGAC 2220
ACTTGGGATT CTCAGACTGT GGACAGGAGT GTTTGTCAAT TTTCATACTG TTTTCTTAAT 2280
AAGCGCTCAG GCCTAAGGTG TGACAGGAAG TCGCACGCGC TTGGCCAGAG CACAGTGAAG 2340
CAAAGGACTG GGTGCTGATG GATGGAGCCA CGGCGGCATC TGCCCACCCG GCCGCAGCCC 2400
CCAGTGCCTC TCCTGGTGGT CCTCCCAGTC TAGAGGGTCA CGGCCCCCCC GCCCTCCTCC 2460
GTCTCTGGCA AGCTGACCTT GACTAACCCA GGAATACAGG GTCATCCTCA TTCCTAAGTA 2520
AGTCAAACAG CAAGACATGG TTTGCGCGGG TCTTTGCCGG AAGCCGGTCC TGCTGGCCAG 2580
GTGTTTTACG TCAGCAGGGA AATGTGGCAC ACGCCCTCGA GGCATTTTAA CACTGTGCTT 2640
CAGGAAATCT CAAGTTCCAT CTTGTGTTAG TAACGTACCC ACATTTTGCT GGAGTTAGTT 2700
TATTAAAGAT GCCTACGGTG AACTCTCTGG CGCAGGTAA ATGCAGTTTT GAAAACCTGG 2760
AAACATCAAA TGGAGGCGGG AAATAGGCTG GGGCCGAGCT GAGGGGCTGA ACACAGCAGT 2820
GACCGTGGGT CAGCAGGTCG CCTGCCCAGC AGGCCCCCA GGAGAGGGCT CGGGCGCCCC 2880
TGGCAGCCCC CATACCCCCA GGACCTGGCT CGTGAGTGCG TCTGGGTCAG GAAGAGACCT 2940
CTCTGTGCGT CTCAGGCTGA GATGCAGATT TCTGTTTTCT AAAACTGGAA GCGACCTTGA 3000
CGTGTATTGA AGGTGTGTGT GCCAAATGCT TCCGACGGAG GTGCTGGCCT TGGTTGGTTT 3060
CTCTCTGCCC CGTGTGGTCA TCAAGTCCTG GGGGATGTGC TCTGCCCAGC CGCCCTCGGG 3120
GAGAGCAGCG CCGCCTCCCA TGGGGCCGTG GGGCTGCTGT TCTCACTGCA CTGGCTGAAG 3180
CAACCCGCCA GCCTCCGTGC CCCACCCAC CCAGCACGCA CTCATTCACT CCATTGCCTT 3240
AACACAAGCC TGATGGGGCT GTTTTCTCAC AATATAAAG AATAAAGTGT CTTCTGGCCT 3300
ACTTCTGAAT TACTTCTCAA CTGTATGGTT TGGGGAAGGG AGGGAAACCT AAAATCCCGT 3360
CCAAATAAGT GAAATTCCTG AAGAAGTGGC TGAGTCCTAC CAGGTGGGG TTAGGGAAAT 3420
GTTCTGGGTT CAGGCGCCCC TCCCAGGGCT GAGAAAGCGC AGCCAGGGAC AGCTTTCTGT 3480
TCTCTCCCAG GGTGGCTAGG TTAGTATCTT ACATGACAAA AACTGAGAG TGTTCTAACT 3540
TCTGTGCAAG CAAGTTAAT CCTGAGACTA AATCTTGGCG TTCAGACTCC CGTAGAGGTC 3600
ATCTGTGTCC AGGCCACCC GGGCGCCGGC TCA 3633

(2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2018 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGTUT13
- (B) CLONE: 3116522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151 :

TGGCTCGCTG GCCGCTCCTG GAGGCGGCGG CGGGAGCGCA GGGGGCGCGC GGCCCGGGGA 60
 CTCGCATTCC CCGGTTCCCC CTCCACCCCA CGCGGCCTGG ACCATGGACG CCAGATGGTG 120
 GGCAGTGGTG GTGCTGGCTG CGTTCCCCTC CCTAGGGGCA GGTGGGGAGA CTCCCGAAGC 180
 CCCTCCGGAG TCATGGACCC AGCTATGGTT CTTCCGATTT GTGGTGAATG CTGCTGGCTA 240
 TGCCAGCTTT ATGGTACCTG GCTACCTCCT GGTGCAGTAC TTCAGGCGGA AGAACTACCT 300
 GGAGACCGGT AGGGGCCTCT GCTTTCCCCT GGTGAAAGCT TGTGTGTTTG GCAATGAGCC 360
 CAAGGCCTCT GATGAGGTTT CCCTGGCGCC CCGAACAGAG GCGGCAGAGA CCACCCCGAT 420
 GTGGCAGGCC CTGAAGCTGC TCTTCTGTGC CACAGGGCTC CAGGTGTCTT ATCTGACTTG 480
 GGGTGTGCTG CAGGAAAGAG TGATGACCCG CAGCTATGGG GCCACAGCCA CATCACCGGG 540
 TGAGCGCTTT ACGGACTCGC AGTTCCTGGT GCTAATGAAC CGAGTGCTGG CACTGATTGT 600
 GGCTGGCCTC TCCTGTGTTT TCTGCAAGCA GCCCCGGCAT GGGGCACCCA TGTACCGGTA 660
 CTCCTTTGCC AGCCTGTCCA ATGTGCTTAG CAGCTGGTGC CAATACGAAG CTCTTAAGTT 720
 CGTCAGCTTC CCCACCCAGG TGCTGGCCAA GGCCTCTAAG GTGATCCCTG TCATGCTGAT 780
 GGGAAAGCTT GTGTCTCGGC GCAGCTACGA ACACTGGGAG TACCTGACAG CCACCCTCAT 840
 CTCCATTGGG GTCAGCATGT TTCTGCTATC CAGCGGACCA GAGCCCCGCA GCTCCCCAGC 900
 CACCACACTC TCAGGCCTCA TCTTACTGGC AGGTTATATT GCTTTTGACA GCTTCACCTC 960
 AAAGTGGCAG GATGCCCTGT TTGCCTATAA GATGTCATCG GTGCAGATGA TGTTTGGGGT 1020
 CAATTTCTTC TCCTGCCTCT TCACAGTGGG CTCACTGCTA GAACAGGGGG CCCTACTGGA 1080
 GGAACCCGC TTCATGGGGC GACACAGTGA GTTTGCTGCC CATGCCCTGC TACTCTCCAT 1140
 CTGCTCCGCA TGTGGCCAGC TCTTCATCTT TTACACCATT GGGCAGTTTG GGGCTGCCGT 1200
 CTTACCATC ATCATGACCC TCCGCCAGGC CTTTGCCATC CTTCTTTCCT GCCTTCTCTA 1260
 TGGCCACACT GTCAGTGTGG TGGGAGGGCT GGGGGTGGCT GTGGTCTTTG CTGCCCTCCT 1320
 GCTCAGAGTC TACGCGCGGG GCCGTCTAAA GCAACGGGGA AAGAAGGCTG TGCCTGTTGA 1380

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GTCTCCTGTG CAGAAGGTTT GAGGGTGGAA AGGGCCTGAG GGGTGAAGTG AAATAGGACC 1440
CTCCCACCAT CCCCTTCTGC TGTAACCTCT GAGGGAGCTG GCTGAAAGGG CAAAATGCAG 1500
GTGTTTTCTC AGTATCACAG ACCAGCTCTG CAGCAGGGGA TTGGGGAGCC CAGGAGGCAG 1560
CCTTCCCTTT TGCCTTAAGT CACCCATCTT CCAGTAAGCA GTTTATTCTG AGCCCCGGGG 1620
GTAGACAGTC CTCAGTGAGG GGTTTTGGGG AGTTTGGGGT CAAGAGAGCA TAGGTAGGTT 1680
CCACAGTTAC TCTTCCCACA AGTTCCCTTA AGTCTTGCCC TAGCTGTGCT CTGCCACCTT 1740
CCAGACTCAC TCCCCTCTGC AAATACCTGC ATTTCTTACC CTGGTGAGAA AAGCACAAGC 1800
GGTGTAGGCT CCAATGCTGC TTTCCCAGGA GGGTGAAGAT GGTGCTGTGC TGAGGAAAGG 1860
GGATGCAGAG CCCTGCCCAG CACCACCACC TCCTATGCTC CTGGATCCCT AGGCTCTGTT 1920
CCATGAGCCT GTTGCAAGTT TTGGTACTTT AGAAATGTAA CTTTTTGCTC TTATAATTTT 1980
ATTTTATTAA ATTAAATTAC TGCAGTGGAA AAAAAAAA 2018

(2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 942 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGTUT13
- (B) CLONE: 3117184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152 :

CCTCCATCAG CTCGCCGCGC AGCGGCTGTA TTTGCGGCCT GTGCGAGTAG GCGCTTGGGC 60
ACTCAGTCTC CCTGGCGGGC GACGGGCAGA AATCTCGAAC CAGTGGAGCG CACTCGTAAC 120
CTGGATCCCA GAAGGTCGCG AAGGCAGTAC CGTTTCCTCA GCGGCGGACT GCTGCAGTAA 180
GAATGTCTTT TCCACCTCAT TTGAATCGCC CTCCCATGGG AATCCCAGCA CTCCCACCAG 240
GGACCCACCC CCCGCAGTTT CCAGGATTTT CTCCACCTGT ACCTCCAGGG ACCCCAATGA 300
TTCCTGTACC AATGAGCATT ATGGCTCCTG CTCCGACTGT CTTAGTACCC ACTGTGTCTA 360
TGTTTGAAA GCATTTGGGC GCAAGAAAGG ATCATCCAGG CTTAAAGGCT AAAGAAAATG 420
ATGAAAATTG TGGTCCTACT ACCACTGTTT TTGTTGGCAA CATTTCCGAG AAAGCTTCAG 480
ACATGCTTAT AAGACAACCT TTAGCTAAAT GTGGTTTGGT TTTGAGCTGG AAGAGAGTAC 540
AAGGTGCTTC CGGAAAGCTT CAAGCCTTCG GATTCTGTGA GTACAAGGAG CCAGAATCTA 600
CCCTCCGTGC ACTCAGATTA TTACATGACC TGCAAATTGG AGAGAAAAAG CTA CTCTCGTTA 660

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AAGTTGATGC AAAGACAAAG GCACAGCTGG ATGAATGGAA AGCAAAGAAG AAAGCTTCTA 720
ATGGGAATGC AAGGCCAGAA ACTGTCACTA ATGACGATGA AGAAGCCTTG GATGAAGAAA 780
CAAAGAGGAG AGATCAGATG ATTAAAGGGG CTATTGAAGT TTTAATTCGT GAATACTCCA 840
GTGAGCTAAA TGCCCCCTCA CAGGAATCTG ATTCTCACCC CAGGAAGAAG AAGAAGGAAA 900
AGAAGGAGGA CATTTTCGGC AGATTTCAGT GGGCCCCACTG AT 942

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2060 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LNODNOT05
- (B) CLONE: 3125156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153 :

TCCCCCCTC AGCCTCCCC CCCCCACTG GCATATGGTC CTGCCCCTTC TACCAGACCC 60
ATGGGCCCCC AGGCAGCCCC TCTTACCATT CGAGGGCCCT CGTCTGCTGG CCAGTCCACC 120
CCTAGTCCCC ACCTGGTGCC TTCACCTGCC CCATCTCCAG GGCCTGGTCC GGTACCCCT 180
CGCCCCCAG CAGCAGAACC ACCCCCTTGC CTGCGCCGAG GCGCCGCAGC TGCAGACCTG 240
CTCTCCTCCA GCCCGGAGAG CCAGCATGGC GGCACCTCAGT CTCCTGGGGG TGGGCAGCCC 300
CTGCTGCAGC CCACCAAGGT GGATGCAGCT GAGGGTCGTC GGCCGCAGGC CCTGCGGCTG 360
ATTGAGCGGG ACCCCTATGA GCATCCTGAG AGGCTGCGGC AGTTGCAGCA GGAGCTGGAG 420
GCCTTTCGGG GTCAGCTGGG GGATGTGGGA GCTCTGGACA CTGTCTGGCG AGAGCTGCAA 480
GATGCGCAGG AACATGATGC CCGAGGCCGT TCCATCGCCA TTGCCCCTG CTACTCACTG 540
AAGAACCGGC ACCAGGATGT CATGCCCTAT GACAGTAACC GTGTGGTGCT GCGCTCAGGC 600
AAGGATGACT ACATCAATGC CAGCTGCGTG GAGGGGCTCT CCCCATACTG CCCCCGCTA 660
GTGGCAACCC AGGCCCCACT GCCTGGCACA GCTGCTGACT TCTGGCTCAT GGTCCATGAG 720
CAGAAAGTGT CAGTCATTGT CATGCTGGTT TCTGAGGCTG AGATGGAGAA GCAAAAAGTG 780
GCACGCTACT TCCCCACCGA GAGGGGCCAG CCCATGGTGC ACGGTGCCCT GAGCCTGGCA 840
TTGAGCAGCG TCCGCAGCAC CGAAACCCAT GTGGAGCGCG TGCTGAGCCT GCAGTTCCGA 900
GACCAGAGCC TCAAGCGCTC TCTTGTGCAC CTGCACTTCC CCACTTGGCC TGAGTTAGGC 960
CTGCCCCACA GCCCCAGCAA CTTGCTGCGC TTCATCCAGG AGGTGCACGC ACATTACCTG 1020

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CATCAGCGGC CGCTGCACAC GCCCATCATT GTGCACTGCA GCTCTGGTGT GGGCCGCACG 1080
GGAGCCTTTG CACTGCTCTA TGCAGCTGTG CAGGAGGTGG AGGCTGGGAA CGGAATCCCT 1140
GAGCTGCCTC AGCTGGTGCG GCGCATGCGG CAGCAGAGAA AGCACATGCT GCAGGAGAAG 1200
CTGCACCTCA GGTTCCTGCTA TGAGGCAGTG GTGAGACACG TGGAGCAGGT CCTGCAGCGC 1260
CATGGTGTGC CTCCTCCATG CAAACCCTTG GCCAGTGCAA GCATCAGCCA GAAGAACCAC 1320
CTTCCTCAGG ACTCCCAGGA CCTGGTCCTC GGTGGGGGATG TGCCCATCAG CTCCATCCAG 1380
GCCACCATTG CCAAGCTCAG CATTGCGCCT CCTGGGGGGT TGGAGTCCCC GGTTGCCAGC 1440
TTGCCAGGCC CTGCAGAGCC CCCAGGCCTC CCGCCAGCCA GCCTCCCAGA GTCTACCCCA 1500
ATCCCATCTT CCTCCCAAAC CCCCTTTCCT CCCCCTACC TGAGGCTCCC CAGCCTAAGG 1560
AGGAGCCGCC AGTGCCTGAA GCCCCAGCT CGGGGCCCCC CTCCTCCTCC CTGGAATTGC 1620
TGGCCTCCTT GACCCCAGAG GCCTTCTCCC TGGACAGCTC CCTGCGGGGC AAACAGCGGA 1680
TGAGCAAGCA TAACTTTCTG CAGGCCATA ACGGGCAAGG GCTGCGGGCC ACCCGGCCCT 1740
CTGACGACCC CCTCAGCCTT CTGGATCCAC TCTGGACACT CAACAAGACC TGAACAGGTT 1800
TTGCCTACCT GGTCTTACA CTACATCATC ATCATCTCAT GCCCACCTGC CCACACCCAG 1860
CAGAGCTTCT CAGTGGGCAC AGTCTCTTAC TCCCATTCTT GCTGCCTTTG GCCCTGCCTG 1920
GCCCAGCCTG CACCCCTGTG GGGTGGAAT GTACTGCAGG CTCTGGGTCA GGTTCCTGCTC 1980
CTTTATGGGA CCCGACATTT TTCAGCTCTT TGCTATTGAA ATAATAAACC ACCCTGTTCT 2040
GTGAAAAAAAA AAAAAAAAAAG 2060

(2) INFORMATION FOR SEQ ID NO: 154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2065 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGTUT12
- (B) CLONE: 3129120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154 :

CGGGTCCCCG GGTCTGACAG GAGCAGCCTG TGGGCACCGC GCGGTTAGTT GGAGGCGGGA 60
GAGGGTCCGT AGCCGCGCCG CCCTGCCCCG CCATGGGCCTT CCTGTCGGAC CCGGTTTCGCC 120
GGCGCGCGCT CGCCCGCCTA GTGCTGCGCC TCAACGCGCC GTTGTGCGTG CTGAGCTACG 180
TGGCGGGCAT CGCCTGGTTC TTGGCGCTGG TTTTCCCGCC GCTGACCCAG CGCACTTACA 240

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TGTCGGAGAA CGCCATGGGC TCCACCATGG TGGAGGAGCA GTTTGCGGGC GGAGACCGTG 300
CCCGGGCTTT TGGCCGGGAC TTCGCCGCC ACCGCAAGAA GTCGGGGGCT CTGCCAGTGG 360
CCTGGCTTGA ACGGACGATG CGGTCACTAG GGCTGGAGGT CTACACGCAG AGTTTCTCCC 420
GGAAACTGCC CTTCCCAGAT GAGACCCACG AGCGCTATAT GGTGTCGGGC ACCAACGTGT 480
ACGGCATCCT GCGGGCCCCG CGTGCTGCCA GCACCGAGTC GCTTGTGCTC ACCGTGCCCT 540
GTGGCTCTGA CTCTACCAAC AGCCAGGCTG TGGGGCTGCT GCTGGCACTG GCTGCCCACT 600
TCCGGGGGCA GATTTATTGG GCCAAAGATA TCGTCTTCCT GGTAACAGAA CATGACCTTC 660
TGGGCACTGA GGCTTGGCTT GAAGCCTACC ACGATGTCAA TGCTACTGGC ATGCAGTCGT 720
CTCCCCTGCA GGGCCGAGCT GGGGCCATTG AGGCAGCCGT GGCCCTGGAG CTGAGCAGTG 780
ATGTGGTCAC CAGCCTCGAT GTGGCCGTGG AGGGGCTTAA CGGGCAGCTG CCCAACCTTG 840
ACCTGTCTAA TCTCTTCCAG ACCTTCTGCC AGAAAGGGGG CCTGTTGTGC ACGCTTCAGG 900
GCAAGCTGCA GCCCGAGGAC TGGACATCAT TGGATGGACC GCTGCAGGGC CTGCAGACAC 960
TGCTGTCTCAT GGTCTGCGG CAGGCCTCCG GCCGCCCCCA CGGCTCCCAT GGCCTCTTCC 1020
TGCGCTACCG TGTGGAGGCC CTAACCCTGC GTGGCATCAA TAGCTTCCGC CAGTACAAGT 1080
ATGACCTGGT GGCAGTGGGC AAGGCTTTGG AGGGCATGTT CCGCAAGCTC AACCACCTCC 1140
TGGAGCGCCT GCACCAGTCC TTCTTCTCT ACTTGCTCCC CGGCCTCTCC CGCTTCGTCT 1200
CCATCGGCCT CTACATGCCC GCTGTCGGCT TCTTGCTCCT GGTCTTGGT CTCAAGGCTC 1260
TGGAACTGTG GATGCAGCTG CATGAGGCTG GAATGGGCCT TGAGGAGCCC GGGGGTGCCC 1320
CTGGCCCCAG TGTACCCCTT CCCCCATCAC AGGGTGTGGG GCTGGCCTCG CTCGTGGCAC 1380
CTCTGTGTGAT CTCACAGGCC ATGGGACTGG CCCTCTATGT CCTGCCAGTG CTGGGCCAAC 1440
ACGTTGCCAC CCAGCACTT CCAGTGGCAG AGGCTGAGGC TGTGGTGTG ACACTGCTGG 1500
CGATTTATGC AGCTGGCCTG GCCCTGCCCC ACAATACCCA CCGGGTGGTA AGCACACAGG 1560
CCCCAGACAG GGGCTGGATG GCACTGAAGC TGGTAGCCCT GATCTACCTA GCACTGCAGC 1620
TGGGCTGCAT CGCCCTCACC AACTTCTCAC TGGGCTTCCT GCTGGCCACC ACCATGGTGC 1680
CCACTGCTGC GCTTGCCAAG CCTCATGGGC CCCGGACCCT CTATGCTGCC CTGCTGGTGC 1740
TGACCAGCCC GGCAGCCACG CTCCTTGGCA GCCTGTTCCCT GTGGCGGGAG CTGCAGGAGG 1800
CGCCACTGTC ACTGGCCGAG GGCTGGCAGC TCTTCTTGGC AGCGCTAGCC CAGGGTGTGC 1860
TGGAGACCA CACCTACGGC GCCCTGCTCT TCCCACTGCT GTCCCTGGGC CTCTACCCCT 1920
GCTGGCTGCT TTTCTGGAAT GTGCTCTTCT GGAAGTGAGA TCTGCCTGTC CGGGCTGGGA 1980
CAGAGACTCC CCAAGGACCC CATTCTGCCT CCTTCTGGGG AAATAAATGA GTGTCTGTTT 2040
CAGCAGCTAT TTGATGCTTG TCACA 2065